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; Search time 46.76 Seconds (without alignments) 1308.014 Million cell updates/sec
                       Sequence 5, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 1, Appli
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Sequence 6, Appli
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Sequence 1, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 20, Appli
                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/051,969A

FILING DATE: 198-09-30

CLASSIFICATION #1.30

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: FLESHNER, RAZ E.

NAME: FLESHNER, RAZ E.

REGISTRATION NUMBER: 0652.169000

TELECOMMUNICATION INFORMATION:

TELEPAN: 202-371-2540

INFORMATION FOR SEQ ID NO: 5:

CROSTENCE CHARACTERISTICS:
                                                     ;
US-09-051-969A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-09-051-969A-5
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4444444
3353333344
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5433554
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APPLICANT: GANNON, FRANK
APPLICANT: BERGEMANN, KLAUS
APPLICANT: NOE, WOLFGANG
TITLE OF INVENTION: INTENSIVE HOMOLOGOUS PROMOTER OBTAINED
TITLE OF INVENTION: FROM HAMSTERS
NUMBER OF SEQUENCES: 8
                                                                                                  MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                           STRANDEDNESS: bot
                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                     NAME/KEY:
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US-08-961-810-17
US-08-961-810-17
US-08-352-902D-17
US-08-238-163-3
US-08-238-163-3
US-08-250-975-8
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US-08-950-449A-8
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Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Match

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Description

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22222221111111 202222211111111 70543210987

2529 579 579 11594 11724 11724 11724 11724 11725 2664 26663 32552 26663 32552 26663 279 279 279 26684

US-09-051-969A-5
US-09-146-950-19
US-09-146-950-19
US-09-146-950-17
US-09-146-950-17
US-09-146-950-11
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US-09-33-279-1
US-09-33-279-6
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Minimum DB Maximum DB

seq length: 0
seq length: 2000000000

Potal number of hits satisfying chosen parameters:

767066

383533 seqs, 122816752 residues

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Perfect score:

US-09-757-781-21 249

Run on: OM nucleic

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

September 20, 2002, 04:43:36;

Post-processing: Minimum Match 0%

Issued_Patents_NA: *

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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Dackfiles1.seq:*

Maximum Match 100% Listing first 45 summaries

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RESULT 3
US-09-146-950-3/c
; Sequence 3, Application US/09146950A
; Patent No. 6287808
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; LCCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C
US-09-328-111-579
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APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENERAL FILLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-328-111-579/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astel, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 579
LENGTH: 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 579, Application US/09328111 Patent No. 6262333 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                        412
                                                                                                                         139 ctgtgaatcccgatgtggaaaagcttggaggtgaaagctcagcataccatgtatttactt 198
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                                                                                                     TTAAACCANCAGAAAAAACGTATATTGGCAGATGTATGTTTT
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Pred. No. 0.039;
0; Mismatches 44;
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                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo
US-09-146-950-19
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US-09-146-950-19/c
Sequence 19, Application US/09146950A
Patent NO. 6287808
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version SEQ ID NO 3 LENGTH: 579
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/146,950A CURRENT FILING DATE: 1998-09-03
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                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 591
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361
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                                                                                                                                                               53 gggtctcggggatctcggtggctcccatcttccttcattgttctgaacatcctgtattgt 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 gggtctcggggatctcggtggctcccatcttccttcattgttctgaacatcctgtattgt 112
                                                                                                                                                                                                                     Local Similarity
les 74; Conserv
                                                                                         aaaccatggctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtga 172
                               aagctcagcataccatgtatttact 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aaaccatggctggggtgctaaagtgcctgtgaatcccgatgtggaaaaaagctggaggtga 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTGTCCTGACTCTCGGTGCCTCCCTTCTGCACCCTCTGGCCCGGGCTGGAGGTGGCGT 422
                                                                   AAGCGCGGCACGCGCACTGGTCCCCGTCCTGGACGATGCAGAAGTGGCCTGGGCTGC
                                                                                                                                             GGGTGTCCTGACTCTCGGTGCCTCCCTTCTGCACCCTCTGGCCCGGGCTGGAGGTGGCGT
AGCCACACACGGCGTTCTCTGTCCT
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51.0%;
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                                                                                                                                                                                                                                       Score 31.4; DB Pred. No. 0.63;
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337
                                                                                                                                                                                                                       Mismatches
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RESULT 5 US-09-146-950-17/c · Sequence 17, Application US/09146950A

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-950-17
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Best Local Similarity
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RESULT 7
US-09-333-279-1/c
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Best Local Similarity
Matches 74; Conserv
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LENGTH: 1724
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TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: PROTEIN FAMILY AND USES
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
UNMBER OF SEQ ID NOS: 25
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APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
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Pred. No. 1.1;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
US-09-333-279-1
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US-09-146-950-1/c
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SEQ ID NO 1
LENGTH: 1929
TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
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TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
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APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEIVED BY THE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/333,279
CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (29
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Local Similarity 51.0%;
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AGCCACACGCGGGGTTCTCTGTCCT
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74; Conservative
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; TYPE: DNA
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US-09-333-279-6
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Best Local S
Matches 74
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Best Local Similarity 51.0%;
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Patent No. 6303336
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CURRENT FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
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APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
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CURRENT FILING DATE: 1999-06-15
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Pred. No. 1.7;
0; Mismatches 71;
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Pred. No. 1.7;
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US-08-539-304A-5
                                                                   Sequence 3, Application US/08136743B Patent No. 5459063 GENERAL INFORMATION:
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Best Local Similarity
Matches 43; Conserv
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TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
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FILING DATE: 04-OCT-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
APPLICANT: Barry S. Cooperman, Harvey Rubin, APPLICANT: Jerome Salem, and Alison L. Fisher TITLE OF INVENTION: "Plasmodium falciparum RibonuTITLE OF INVENTION: cleotide Reductase, DNA Sequen
                                                                                                                                                                                            1761 TTTA 1764
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: 23
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join(741..1093,
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Pred. No. 2.8;
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     DNA Sequences Therefor and
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     Peptide inhi
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

The University of Pennsylvania

STREET: Suite 330
STREET: 3700 Market Street

TITLE OF INVENTION:

Thereof"

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                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09118442B Patent No. 6197561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                              EARLIER APPLICATION NUMBER: 60/055,526
EARLIER FILING DATE: 1997-08-08
EARLIER APPLICATION NUMBER: 60/053,944
EARLIER FILING DATE: 1997-07-28
                                                                                            TITLE OF INVENTION: Genes Controlling Phytate Metabolism in TITLE OF INVENTION: Plants and Uses Thereof FILE REFERENCE: 0706
CURRENT APPLICATION NUMBER: US/09/118,442B
CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/055,446
EARLIER FILING DATE: 1997-08-11
SOFTWARE: FastSEQ
                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                          APPLICANT: Wang, Hongyu
APPLICANT: Beach, Larry
                                                                                                                                                                                                           APPLICANT: Wang, Xun
APPLICANT: Bowen, Benjamin A.
                                                                                                                                                                                                                                                                            APPLICANT: Martino-Catt, Susan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: NO. 5459063e INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2241 ATTTTTTTTTT
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176
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                                                                                                                                                                                                                                                                                                                                                                                                                                            236 ttttttttatt 247
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REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 10/14/
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TELEFAX: (215) 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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19104-3246
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for Windows Version 3.0
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63.9%;
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1862 GTTCAAGGCACTCTTAAATATAGACGATTCTTGAGGCACAACTCCTGTTAGGAGAAGAGT 180

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                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: (1)...(3232)
; OTHER INFORMATION: n = A,T,C or
US-09-677-064-1
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                                         Matches
                                                         Query Match
Best Local
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Best Local
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/677,064
CURRENT FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Genes Controlling Phytate Metabolism TITLE OF INVENTION: Plants and Uses Thereof
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                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (258)...(2666)
                                                                                                                                                                                                                     FEATURE:
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TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1)...(3252)

OTHER INFORMATION: n = A,T,C or G
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92 gttctgaacatcctgtattgtaaaccatggctggggtgctaaagtgcctgtgaatcccga 151
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                                                        Local
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les 76; Conserv
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                                         th 12.2%; similarity 50.0%; 76; Conservative
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Beach, Larry R.
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Pred. No. 3;
0; Mismatches
                                          0;
                                       Score 30.4; I
Pred. No. 3;
0; Mismatches
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NAME/KEY:
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FCT-US96-12374-1
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; Sequence 1, Application PC/TUS9612374
; GENERAL INFORMATION:
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Best Local Similarity 50.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1724 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: NOITHIUP, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
TELEPAX: (312) 616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: Dressler, Goldsmith, Milnamow & Katz, Ltd.
ADDRESSEE: Dressler, Goldsmith, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Northwestern University
TITLE OF INVENTION: Herpes Virus Entry Mediator
NUMBER OF SEQUENCES: 5
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                           .173 aagctcagcataccatgtatttact 197
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                                                                    714
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654 AGCCACACGCGCGTTCTCTGTCCT 630
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ZIP: 606
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                    AACGGCGGCACGCGCGCGCAGTGGTCCCCGTCCTGGACGATGCAGAAGTGGCCTGGGCTGC 655
                                                                                                                                                                                                        73; Conservative
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                                                                                                                                                                                                                        Score 29.8; DB 5; Pred. No. 3.5;
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Search completed: September 20, 2002, 05:55:09 Job time: 4293 sec

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ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS RESULT 1 AI079538/c COMMENT FEATURES DEFINITION ACCESSION Locus TITLE JOURNAL source 536 bp mRNA linear EST 29-SEP-ioz04e06.xl Soares_fetal_liver_spleen_lNFLS_Sl Homo sapiens cDNA clone TMAGE:1674370 3', mRNA sequence. Mammalia; Eutheria; Primates; Catarrilli, nom

1 (bases 1 to 536)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL CANOMIC ANALYSIS ANALYSI Tumor Gene Index Unpublished (1997) Eukaryota; Metazoa; Homo sapiens human. AI079538.1 GI:3415789 National Cancer Institute, Cancer /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (amplicillin resistant)"
/note="07gan: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGB:1674370" /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1" double-stranded cDNA was ligated to /sex="male" Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae; Genome Anatomy Project (CGAP), Hominidae; Eco RI adaptors Euteleostomi; EST 29-SEP-1998 Homo

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1 (bases 1 to 536)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
AI497808
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tm89f02.xl NCI_CGAP_Brn25 Homo
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Insert Length: 779 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
cound through the I.M.A.G.E. Consortium/LLNL at:
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/clone="IMAGE:2165307"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic ol
/lab_host="DH10B"
                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                         Luxaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 561)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. ·
National Cancer Institute, Cancer Genome Anatomy Proj Tumor Gene Index
[Innuhliable] '''
                                                                                                                                         AI038061
AI038061.1
                                                                                                                                                                                                                                                                                                                                                                                           ox21b05.x1 Soares_fetal_liver_spleen_lnFLS_S1 Homo clone IMAGE:1656945 3', mRNA sequence.
                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                           human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="0rgan: Liver and Spleen, Vector: pT
with a modified polylinker; Site_1: Pac I;
                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1656945"
                                                     /sex="male"
                                                                 /clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     GI:3277255
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Pred. No. 1.1e-51;
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                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
BF679962
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602154666F1 NIH_MGC_83 Homo
                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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1 (bases 1 to 626)
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                                                                                                                                          Plate: LLCM1146 row: d column: 17 High quality sequence stop: 621.
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National Institutes of Health, Mammalian
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/clone="IMAGD: #22222"
/clone_lib="NIH_MGC_883"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Clontech);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        liver spleen 1NFLS library. 1st strand with a Pac I - oligo(dT) primer [5'
                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4295392"
                                                                                                                            Location/Qualifiers
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Pred. No. 1.1e-51;
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Local Similarity 99.6%;
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE176440
RC3-HT0585-160300-022-d04
BE176440
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0585-160300-022-d04&t3=2000-03-16&t4=1)
                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Rese
Rua Prof. Antonio Prudente 109;
                                                                                                                                                                                                                                                                                        sequence tags
                                                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                              Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                      Email: asimpson@ludwig.org.br
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                                                                                                       +55-11-2704922
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                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGACAGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:8639169
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HT0585 Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW242451 S40 bp mRNA linear EST 14-DEC-1999 aW242451 NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2692302 3',
                                   CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hom

1 (bases 1 to 540)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
AW242451
 Seq primer: -400P from Gibco High quality sequence stop: 4
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Mammalia; E
                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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sequence stop: 463
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98.4%;
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Primates;
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Pred. No. 4.2e-50;
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                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 486)
                                                                                                                                                                                                                                                                                                       3', mRNA sequence.
AI333325
                                                                                                                                   Tumor Gene Index
Unpublished (1997)
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                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                           quality sequence stop: 447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fatima Bonaldo. "
113 g
Location/Qualifiers
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/db_xref="taxon:9606"
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98.0%;
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Pred. No. 1.1e-49;
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sapiens cDNA clone
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source
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                                                                                          Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prang
I.M.A.G.E. Consortium DNA Sequencing by: Washington Unive
                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AI952086
AI952086.1 GI:5744396
          www-bio.llni.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 413.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, 1 (bases 1 to 486)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_NhHMPu_S1"
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100.0%;
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Pred. No. 1.1e-48;
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IMAGE:2546756 3',
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                                                                                                                                                                         Prange, The
                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 444. Cocation/Qualifiers 1..545
                                                                                                                                                                                                                                                   Tumor Gene Index Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
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                                             /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not
Site_2: Eco RI; 1st strand cDNA was primed with a Not
oligo(dT) primer [5'
                                           oligo(dT) primer
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."

112 c 100 g 110 t
                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                          /lab_host-"DH10B"
                                                                                                        /dev_stage="adult"
                                                                                                                        /sex="female"
                                                                                                                                    /clone="IMAGE:1713028"
/clone_lib="Soares_pregnant_uterus_NbHPU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGATCTCGGTGGCTCCCATCTTCCATGGTTTTGACCATCCTGTATTGTAAACCAT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246;
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1 (bases 1 to 687)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Magai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-HT0585-010
400-013-b05&t3=2000-04-01&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                sequence tags
                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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46; Conservative
                                                                      quality sequence start: 13 quality sequence stop: 657.
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                                                                                                                                                                                                                                   +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                           Natl. Acad.
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128 c 116 g 129 t
                                                    Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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NCI/NNIDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI/NNIDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute / National Institute of Neurole Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (DISDIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                qy65f11.x1 NCI_CGAP_Brn25
mRNA sequence.
AI356239
                              CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/tmage.html
Insert Length: 770 Std Error: 0.00
Seq primer: -40UP from Gibco
                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N.
                                                                                                                                                                                                                                                                                                                                                                                                                                AI356239.1
                                                                                                                                                 Bonaldo,
                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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46; Conservative
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sonaldo, Ph.D.
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quality sequence stop: 'Location/Qualifiers'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: head_neck; vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="HT0585"
                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:4107860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.78;
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Pred. No. 8.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                   Louis,
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                                                                                                                                                                                                   Myrna R.
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                                                                                                                                                                    Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 16-FEB-1999
IMAGE:2016909 3',
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                                                                                                                                                                                                                                                                                                   Neurological
                                                                                                                                                                      3
                                                                                                                                                                                                     Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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                                                                                                                                                                      Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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REFERENCE
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ORGANISM
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
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Best Local Similarity
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                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 CTGAACATCCTGTATTGTAAACCATGGCTGGGGTGCTAAAGTGCCTGTGAATCCCGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggaaaaagctggaggtgaaagctcagcataccatgtatttactttaaaaacagaaaaaaa 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctgaacatcctgtattgtaaaccatggctggggtgctaaagtgcctgtgaatcccgatgt 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215;
                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 462)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI309934
qo71e02.x1 NCI_CGAP_Kid5
mRNA sequence.
AI309934
                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
Insert Length: 1094 Std Error: 0.00
                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI309934.1 GI:4004805
EST.
                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                 Insert Length: 1094 Std Err
Seg primer: -40UP from Gibco
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                                              quality sequence stop: 425
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="iMAGE:2016909"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 215; DB 9; Pred. No. 3.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 bp mRNA linear EST 01-FEB-1999 Homo sapiens cDNA clone IMAGE:1913978 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                              Genome Anatomy Project (CGAP),
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AI369277/c
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                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 atggatatgtctattttttttttttttgg 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 TCCTGTATTGTAAACCATGGCTGGGGTGCTAAAGTGCCTGTGAATCCCGATGTGGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 tcctgtattgtaaaccatggctggggtgctaaagtgcctgtgaatcccgatgtggaaaaa 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 446)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurole Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                             CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 723 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI369277
446 bp mRNA linear EST 17-MAR-1999
qy91b11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2019357 3',
                                                                                                                                                                                                            Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N.
                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI369277.1 GI:4148030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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                                                                                                                                                                                                                            cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructed by Bento Soares and M. Fatima Bonaldo. 105\ c 92\ g 108\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1913978"
/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.5%; Score 208; DB 9; 100.0%; Pred. No. 1.7e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                    N. Louis,
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                                                                                                                                                                                                                                                                  M.D., Myrna R.
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                                                                                                                                                    information can be
                                                                                                                                                                      Sequencing Center
                                                                                                                                                                                                                              M. Fatima
                                                                                                                                                                                                                                                                    Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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RESULT 14
AI192867/c
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KEYWORDS
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AUTHORS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 taaaccatggctggggtgctaaagtgcctgtgaatccccgatgtggaaaaagctggaggtg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaagctcagcataccatgtatttactttaaaaaacagaaaaaaagacatgtatggatatgt 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTATTTTTTTTTTTTGG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctattttttttttttgg 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAACCATGGCTGGGGTGCTAAAGTGCCTGTGAATCCCGATGTGGAAAAAGCTGGAGGTG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGTCTCGGGGATCTCGGTGGCTCCCATCTTCCTTCATTGTTCTGAACATCCTGTATTG 387
                                                                                                                                                                                                                                                                                                                                                                                                         436 bp mRNA linear EST 29-00 qe68b05.xl Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744113 3', mRNA sequence.
                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      AI192867.1 GI:3744076
                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                       (bases 1 to 436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.5%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone-"IMAGE:1744113"
/clone_lib-"Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
                                                    /lab_host="DH10B (ampicillin resistant)"
                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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s 0;
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                                                                                                                                                                                                                                                                          Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 29-OCT-1998
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                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
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AA293275/c
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4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 427)
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AA293275
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2t38e06.sl Soares ovary tumor
IMAGE:724642 3' similar to con
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/db_xref="GDB:5936269"
/db_xref="taxon:9606"
                                    /organism="Homo sapiens'
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Copyright (c) 1993 - 2000 Comp
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DE CERTIFICATION OF THE PRESENTATION OF THE PR RESULT AAF91875 03-SEP-1999; 03-SEP-1999; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; 31-AUG-2000; 2000WO-US24008 WO200118022-A1 Homo sapiens. binding endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive; Parkinson's disease; cognitive disorder; schizophrenia; asthma; inmune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Human; Human secreted protein-encoding gene 18 cDNA clone HFPFK57, 22-MAY-2001 (first entry) AAF91875; AAF91875 standard; cDNA; 867 15-MAR-2001. foetal secreted protein; proliferative disorder; cancer; tumour; partner 99US-0152315. 99US-0152317. identification; developmental abnormality; haematopoietic disorder; ВP

SEQ ID NO:28.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted protein genes, and AAB87342-AAB87413 represent the proteins they encode. AAB87414-AAB87454 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein to a protein secreted by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's
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                                                          tttattgg
                                                                                                                                              Cataccatgtatttactttaaaaacagaaaaaaagacatgtatggatatgtctattttt
                                                                                                                                                                                                                                                                      gctggggtgctaaagtgcctgtgaatcccgatgtggaaaagctggaggtgaaagctcag
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                                                                                                                                                                                                                                    gctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtgaaagctcag
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                                                                                                                                                                                                                                                                                                                                                                                     gggatctcggtggctcccatcttccttcattgttctgaacatcctgtattgtaaaccatg
                                                                                                                  cataccatgtatttactttaaaaaacagaaaaaaagacatgtatggatatgtctattttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young PE, Ebner R,
Shi Y, Wei Y, Flore
                                                             249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fiscella M,
R, Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
2.9e-65;
s 0;
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Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>_</u>
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Lafleur DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               867;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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AAH73337
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Best Local Similarity
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                                                                                                                                                                    4914
                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for install cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cervical cancer marker nucleic acid 4611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH73337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-2000;
12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2001
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 241
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                                  cataccatgtatttactttaaaaacagaaaaaaaagacatgtatggatatgtctattttt
                                                                                  | gctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtgaaagctcag
                                                                                                                     gggatctcggtggctcccatcttccttcattgttctgaacatcctgtattgtaaaccatg
                                                                                                                                 gggatctcggtggctcccatcttccttcattgttctgaacatcctgtattgtaaaccatg
                                                                                                                                                                 for assessing and detecting compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated nucleic acid for diagnosing and treating cervical cancer
                      cataccatgtatttactttaaaaaacagaaaaaaagacatgtatggatatgtctattttt
                                                                     gctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtgaaagctcag
                                                                                                                                                                                                                  249;
                                                                                                                                                                                                                                                                            5510
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                                                                                                                                                                                                                                                                                                                                                                                                           Page 1029-1031; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                    gene therapy.
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0189315.
2000US-0203791.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0210600
2000US-0220114
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                                                                                                                                                                                                                                                                           BP; 1526 A;
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99US-0171350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic;
                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berger
                                                                                                                                                                                                                                                                            1242 C;
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pre-malignant condition;
                                                                                                                                                                                                                            Score 249; DB 22; Pred. No. 5.7e-65;
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                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                            1418
                                                                                                                                                                                                                                                                           G;
                                                                                                                                                                                                                                                                            1305
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                                                                                                                                                                                                                                                                            19 other;
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RESULT
AREAS
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ADLISA4424
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AAT87468
ID AAT8
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Best Local S
Matches 44
                                                                                                                                                                   5745
                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01ek
   29-JAN-1998
                                                                        AAT87468 standard;
                                                                                                                                                                                                                                                                                                                              Sequence 7784 BP; 1776 A; 134 C; 2219 G;
                                                                                                                                                                                                                                                                                                                                                               macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ALDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisoriatic; antirheumator; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer; disease; AIDS; epilepsy; neuroffbrotectic; antiarthritic; antipoloid leukaemia; Alzheimer; disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5154 ttttattgg 5162
                                     AAT87468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL34424 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
gene, de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic;
                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
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                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO 2397; 32pp + Sequence Listing;
(first entry)
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                                                                        DNA;
                                                                                                                                                                                                                                                      14.5%;
77.2%;
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                                                                        2529
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                                                                                                                                                                                                                                     Score 36.2; Di
Pred. No. 1;
0; Mismatches
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                                                                        ВP
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                                                                                                                                                                                                                                                                                                                              3655 T;
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                                                                                                                                                                                                                                                                     Length 7784;
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abnormal
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prodn. of heterologous
Ovary cells.
                                           Cells containing the promoter of prodn. of heterologous proteins,
                                                                                                                Nucleic acid containing promoter and hamster ubiquitin S27a gene - useful proteins, especially in CHO cells
The promoter has greater transcriptional activity than the herpes simplex thymidine kinase promoter and about the same as the SV40
                                                                                         Claim 4,
                                                                                                                                                                                                                                                                                                                                                                                                                      misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_signal
                                                                                                                                                                               WPI; 1997-246232/23.
                                                                                                                                                                                                                                       (THOM ) THOMAE GMBH KARL
                                                                                                                                                                                                                                                                    24-OCT-1995;
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misc_feature
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                                                                                       25-26; Fig 5;
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813..861
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/note= "polypyrimidine-rich sequence"
2374..2392
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/note= "homology with amplification sequences"
2279. 2302
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/note= "promoter
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739..2400
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/note= "promoter
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/note= "promoter
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/note= "promoter
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                                                                                       22pp; German
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"Spl binding site"
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RESULT 5.
AAF22291/c
ID AAF22291;
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PR 13-SEP-19
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                             The present invention relates to a recombinant DNA construct of a (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clottin factors, cytokines, antibodies, and growth factors.
                                                                                                                                             Claim 102;
                                                                                                                                                                     Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors \mathbf{f}_i the construction of transgenic plant and animal cells -
                                                                                                                                                                                                                                         WPI; 2000-587529/55.
                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAR-2000; 2000WO-US07392
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                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1999;
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99US-0153584.
99US-0154603.
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139 ctgtgaatcccgatgtggaaaagctggaggtgaaagctcagcataccatgtatttactt 198

Query Match Best Local Matches

Similarity

14.1%;

Score 35.2; DB Pred. No. 0.79;

DВ

21;

619; 0;

Conservative

0;

Mismatches

44;

Indels Length

Gaps

0

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RESULT 6
AAZ80495/c
ID AAZ804
XX AAZ804
XX AAZ804
XX AAZ804
XX AAZ804
XX Human
XX Human;
KW Colore
KW Cytost
KW Hyperp
XX Homo s
XX Homo
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                                                AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The CDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia, dysplasia or hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endege WO,
Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene expression product; diagnosis; tumour; colon cancer colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
     Sequence
                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 361; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               particularly cancers, especially colon
                                                                                                                                                                                                                                                                                                                                                                                                                             treatment
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Catino TJ,
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     BP;
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Pred. No. 5.
          103
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          215
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d DM, Lewis
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          T; 14 other;
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                                 the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                           AAB95893 represent human am represent oligonucleotides, of the present invani-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota T,
Ishii S,
                                                                                                                                                                              sequence and an oligonucleotide comprising a sequence complementary to polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence, 3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                            of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                      to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                       full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID 16860;
                                                                                                                                                                                                                                                                                                                                                                                                                      full-length cDNAs define and/or diagnosis of the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH17416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH17416 standard; cDNA; 1734 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA sequence SEQ ID NO:16860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199
                                                                                                                                                                                                                                                                                                                                                        present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAAACCANCAGAAAAAACGTATATTGGCAGATGTATGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGTAAATCTGGGTTTAGATGCATCTGTAGGAAGTAGGTAAAGCTGTCAGTTATCTTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                   for synthesizing cDNAs defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection; diagnosis; antisense therapy; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                     describes primer sets for synthesising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hikawa T,
Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                    2537pp +
                                                                                                                                                                                                                                                                                                                                                                                                                               izing polynucleotides, particularly the 5602 ed in the specification, and for the detection abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                         G
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                       ROM;
                                                                                                                                                                                                                                                                                                                                                                                     English
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(, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto J;
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                                     by chromosome 2 of the human malarial parasite, Plasmodium falciparum.

Also described are: (1) nucleotide sequences (11) encoding (1); and (2)

C vaccines against P. falciparum infection comprising (1) or (11).

C (1) and (11) are useful for the development of vaccines against

P. falciparum infection. (1) and polyclonal antisera or a monoclonal

antibody raised to immunogens comprising the sequences of (1), are

useful in the detection of infection with P. falciparum. Furthermore,

(1) (especially when they are rifins or secreted or membrane proteins)

can aid the identification of drugs to treat or prevent P. falciparum

infection, or they can be used to identify drug resistance in

P. falciparum. Sequencing of the Plasmodium chromosome 2 and the

subsequent identification of proteins encoded by it will help to expand

our understanding of parasite biology, a process hampeared by the

complexity of the parasitic lifecycle, and provide new targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
                                                                                                                                                                                                                                                                                                   Proteins encoded by chromosome 2 Plasmodium falciparum, useful as diagnosis of P.falciparum infecti
           complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mover resistance to insecticides have led to a resurgence of malaria in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1413
                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                        Disclosure; Page 558-559;
                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-365347/31
                                                                                                                                                                                                                                                                                                                                                                                                                     (GARD/)
(VENT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimalarial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1353
                                                                                                                                                                                                                                                                                                                                                                                         Hoffman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum; chromosome 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA70246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA70246 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOFF/) HOFFMAN
(CARU/) CARUCCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                            present invention describes proteins and their fragments (I) encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         accatggctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtgaaa 174
                                                                                                                                                                                                                                                                                                                                                                                                   _ARUCCI D.
//) GARDNER M.
//) VENTER J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Carucci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malaria;
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53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2364
                                                                                                                                                                                                                                                                                                                                                                                         Gardner
                                                                                                                                                                                                                                                                      577pp; English
                                                                                                                                                                                                                                                                                                    infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.8; D
Pred. No. 1.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                  of the human antimalarial
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                                                                                                                                                                                                                                                                                                                                                                                       Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human malaria parasite;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence
                                                                                                                                                                                                                                                                                                                   malarial vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                            drugs and mosquito
                                                                                                                                                                                                                                                                                                                  parasite,
and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
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                                                                  to expand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                               macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                     30-JUN-2000;
01-SEP-2000;
                                                                    including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                           Claim 1;
                                                                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                  Olek A,
                                                                                                                                                                                                                                                                                                                                            02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                               WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL34231 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2364 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAATTATCTGCATGAGATGACTTTAATTTATTATCATCAACAATAACATTTTTTTGATAT 1795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                  Piepenbrock C,
                       The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                         ID NO 2204;
                                                                                                                                                                                                                                                                                                    2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system
                    present sequence is a gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1222 A; 247 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
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                                                                                                                                       32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                  Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene SEQ ID NO: 2204
                                                                                                                                                                                                                                                 ζ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682 T; 0 other;
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                      invention.
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RESULT 1
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Best Local
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07-APR-2000;
30-JUN-2000;
                         The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, in the control of the control of
                                                                                                                                                                                                                                                                                                                                               18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-017470/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene regulation-associated gene oligonucleotide #408
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; 2000DE-1043826.
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Pred. No. 4.5;
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macular degeneration, arteriosclerosis, anaemia, cancer, acute mycleukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1966
                                                         The present invention provides a number of human immune system associates genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                  Claim 1;
                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                  Olek
                                                                                                                                                                                                                                                                                                       30-JUN-2000;
01-SEP-2000;
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acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence included in the sequence data for this specification
                                                                                                                                                                                                                                                                           (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurofibromatosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                           methylation
                                                                                                                                                                                                                                               Piepenbrock C,
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2000DE-1043826
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Pred. No. 4.
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Query Match Best Local :

Matches

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                                  A method has been developed for the preparation of hydrogenase in which can blue-green alga introduced by a recombinant vector containing a heterologous hydrogenase gene is cultured in a medium to form and compared by a recombinant vector containing a gene cacumulate hydrogenase in the microbe body. Also claimed are: (1) a blue-green alga introduced by a recombinant vector containing a gene can bright production of the compared production of hydrogenase structural gene derived from a Clostridium genus microbe; (2) a method for the production of hydrogen by culturing the above consisting of amethod for the production of hydrogen by culturing the above containing a gene by culturing the above blue-green alga materologically and then under light irradiation; (4) a method for the production of hydrogen by reacting the above blue-green alga manerobically and then reacting it with an clectron receptor. The method is mild to environment. The present sequence represents a nucleotide sequence from an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparation of heterologous hydrogenase in blue-green algae -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shine-Dalgarno;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium; hydrogenase; blue-green alga; hydrogen; microbe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7784 BP; 1690 A; 134 C;
Sequence 1900
                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ25197 standard; DNA; 1900
                                                                                                                                                                                                                                                                                                        for production of hydrogen and is environmentally friendly
                                                                                                                                                                                                                                                                                                                                                                           (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
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                                                                                                                                                                                                                                                                              Fig 4; 12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
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 B₽;
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741 A;
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                                                                                                                                                                                                                                                                              Japanese
 251
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Pred. No. 4;
0; Mismatches
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 336
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 572 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3861 T;
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RESULT 1

AAS445358

ID AAS445368

ID AAS445368

AXX AAS4

XXX AAS4

XXX Call

KW Call

KW Jammu

KW Jammu

KW Jammu

KW PCR

OS Homc

XXX Homc

XXX 15-1

PR 06-1

PR 07-1

CC 15-1

PR 07-1

CC 20-1

CC 3-1

CC 3-1
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                                                                       Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, asteriosciparatic colid trease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Designing primers and probes for analysing diseases associated cytosine methylation state e.g. arthritis, cancer, aging,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2000;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                graft-versus-host disease; glomerular disease; Lewy body disease; cancer;
arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200168911-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2001; 2001WO-EP02945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS45358 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mmunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pretreated genomic DNA associated with cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                        solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antitumour; cytostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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Sequence 6298

B₽;

1583 A;

182 C; 1402 G;

3131 T;

0 other;

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RESULT 14
AAH10129/c
ID AAH101
XX AAH101
XX AAH101
XX Human
DT 26-JUN
XX Human;
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YX Human;
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Best Local
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of apolynucleotide which comprises a 5'-end complementary strand of apolynucleotide which comprises a 5'-end
                                                                                                                                          sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy: The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the
                           detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID 6964; 2537pp + CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and/or diagnosis of the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA clone
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, Sugiyama'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakama
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56.1%;
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Wakamatsu
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      amino acid sequences;
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A, Nagai K,
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      and AAH13629
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 540 BP; 160 A; 123 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antisoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; ana acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy
                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 152; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A,
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01-SEP-2000; 2000DE-1043826.
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           Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.

NEDO human cDNA sequencing project Unpublished (2000)

(Dases I to 2696)

Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isoga: Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Direct Submission
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Homo sapiens atypical PKC isotyp
variant mRNA, complete cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                       Homo sapiens
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                                                                                                 AF196185.1
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                                                             human.
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Submitted (18-OCT-1999) Laboratory of Molecular and Cellular
Oncology, Shanghai Institutes for Biological Sciences, Chinese
Academy of Sciences, 320 Yue-Yang Road, Shanghai 200031, P.R. C
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Exon/Intron Structure
Polarity Gene, hASIP
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Frang, C.M. and Xu, Y.H.
Down-regulated expression of atypical PKC-binding asip isoforms in human hepatocellular carcinomas Cell Res. 11 (3), 223-229 (2001)
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RRFEQAQHMFRQAMRTPI I WFHYVPAANKEQYEDLSQSEKNNYYSSRFSPDSQYINR
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                     RNGYLGGHGFNARVMLETQELLRQEQRRKEQQMKKQPPSEGPSNYDSYKKVQDPSYAP
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1395 c 1581 g 1358 t 1 others
                                                                                                             NHDRIQRLRQEFQQAKQDEDVEDRRRTYSFEQPWPNARPATQSGRHSVSVEVQMQRQR
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                                                                                                                          gctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtgaaagctcag 180
                                                           GCTGGGGTGCTAAAGTGCCTGTGAATCCCCGATGTGGAAAAAGCTGGAGGTGAAAGCTCAG 5641
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                                                                                                                                                                                             ll Similarity
249; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector sequences.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-DEC-1996) Bioinformatics Division, Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA On Dec 9, 1998 this sequence version replaced gi:1773048.

Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing Technology. Data may contain low quality seq uence and BAC/Cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 22279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U82210 22279 bp DNA linear HTG 30-AUG-2001 Homo sapiens chromosome 10 clone CRI-JC2075 map 10p11.2, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing of Human Chromosome 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                               the accession number will be preserved.

1 22279: contig of 22279 bp i
Location/Qualifiers
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L. and Smith, D.
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                   /map="10p11.2"
/clone="CRI-JC2075"
5238 c 5397 g
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                         /chromosome="10"
                                                                                                                                                                                           0,
                                                                                                                                                                                                       Score 249; DB 2;
Pred. No. 1.8e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL Submitted (18 JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CH10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 19, 2001 this sequence version replaced gi:14625535.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: LMBL; Sw:, Sw:SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP their course of the part of the wormper and the course of the part of the course of the part of the wormper and the course of the part of the wormper and the course of the part of the wormper of the wormper and the course of the part of the wormper and the part of the part of the wormper the wormper and the part of the part of the wormper and the part of the wormper this sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/NGP/Chr10 RP11-406D17 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is not the entire insert of clone RP11-406D17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP13-348N17 is at 104199 in this sequence. The true right end of clone RP11-490024 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL160409
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VECTOR: pBACe3.6
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/note="MIR repeat: matches
1232. .1275
                                                                                                                                                /clone_lib="RPCI-11.2"
27. .160
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                          989. .1039
                                                                                                         /note="MIR repeat: matches
                                                                                                                                                                                                                       /chromosome="10"
/clone="RP11-406D17"
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                                       .144 of
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/note-"22 copies 2 mer ac

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/note="26 copies 2 mer aa 73% conserved" 16133..16443
/note="Alusx repeat: matches 1..312 of consensus" 16599..16707
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/note="MER61E repeat: matches 377. .466 of consensus" 14551. .14771
/note="pTR5 repeat: matches 1874. .8522 of consensus" 14772. .14923
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/note="AluSx repeat: matches 1.
4229. .4606
   /note="AluJo repeat: matches 1.
22502. ,22739
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l7579. .17889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="38 copies 2 mer ta 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MER57B repeat: matches 43. .386 of consensus" 10851. .10975
/note="FLAM_C repeat: matches 15. .133 of consensus" 11451. .11758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10005. .10072
/note="L2 repeat: matches 2673. .2741 of consensus"
10542. .10849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1648: .4815
/note="FRAM repeat: matches 4. .5215. .5516
/note="AluSx repeat: matches 1.
                                                                                                                                                          'note-"AluJb repeat: matches 1.
                                                                                                                                                                                                                note="AluJo repeat: 10333. .20642 repeat: 20542 repeat: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5223. .15519
'note="AluSq repeat: matches 1.
.5661. .15818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161. .6216
/note="MIR_repeat: matches 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MLT1J repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 528. .6637
note="MIR repeat: matches 104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"AluJo repeat: matches 1. .292 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"AluSx repeat: matches 1.
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0005. .10072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    061. .8354
note="AluJb repeat: matches 1. .289 of consensus"
143. .8602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;46. .6950
note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  te="AluSg repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           te="L1MC4_repeat: matches 7728. .7834 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te="AluJb repeat: matches 1.
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92. .14459
                                                                                                                                                                                                                                                                                                                                               te="MLTID repeat: matches 3..238 of consensus"
87..19391
te="AlluG repeat: matches 1..310 of consensus"
92..19342
ne="MLTID repeat: matches 238..501 of consensus"
                                                                                              :e="L2 repeat: matches 2414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em"AluSx repeat: matches 3. .154 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .16787
                                                                                                                                                                                                                       matches 1.
                                                                                                                                                                                                                                                                                      matches 1.
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                                                                                                                                                                                                                                                                                      .295 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .299 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .293 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .312 of
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                              .311 of consensus
                                                                                              .2696 of consensus'
                                                                                                                                                                                                                       .310 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .304 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .300 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .403 of
                                                                                                                                                             .286 of
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                                                                                                                                                             consensus"
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                                                                                                                                        /note="AluSq repeat: n
44991. 45302
/note="AluJo repeat: n
4536. .51640
/note="L1PA7 repeat: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2622...
36582...36804
/note="MER30 repeat: matches 1...
37547...37852
/note="Alusx repeat: matches 1...
37894...38050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSx repeat: matches 1.
23135. .23915
                                                                                         /note="AluJb repeat: 51966. .52183
                                                                                                                                                                                                                   #3386. 43747 repeat: matches 5515. .6138 of consensus" flote="7HEIB repeat: matches 1. 34771 44459. .44771
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/note="L1MA3 repeat:
28661. .28984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="66 copies 2 mer aa 62% conserved"
10233. .30328
'note="48 copies 2 mer ta 65% conserved"
                                                                          note="109"
                                                                                                                                                                                                                                                                                                                                                                                      note="MER5A repeat: matches 9. .188 of consensus"
18447. .38744
18447. .38744
19063. .39193
19063. .39193
19164 TEAM_C repeat: matches 1. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="pTR5 repeat: matches 172. .2212 of consensus"
.4713. .34840
rocte="aludo/FRAM repeat: matches 178. .302 of consensus"
F266
                                                                                                                                                                                                                                                                                                                                        9510. .39673
note="MER5A repeat:
0932. .41102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L1MC4 repeat: matches 6940. .6995 of consensus" 1133. .31547 note="L1MC4 repeat: matches 7167. .7597 of consensus" 1648. .32167
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note="AluJo repeat: matches 1.
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3283. .33415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluJo repeat: matches 5. .282 of consensus" 2592. .32686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1PA10 repeat: matches 5369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="L1PA6 repeat: matches 5612. .6131 of consensus"
2275. .32552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L1MC4 repeat:
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                                                                         copies 2 mer aa 69% conserved'
Score 249; DB 9;
Pred. No. 2e-60;
); Mismatches 0;
                                                                                                                                              matches 11.
                                                                                                                                                                             matches 1.
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                                                                                                                                                                                                                                                                                                                                                         matches 4. .189 of
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                                                                                                           matches 1.
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AC025823/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-MAR-2000) Genome Therapeutics Corporation, Street, Waltham, MA 02453, USA On Apr 27, 2001 this sequence version replaced gi:9887686
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138688 bp DNA linear HTG 24-JAN-2002
HOMO Sapiens chromosome 10 clone RP11-60H16, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                             as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 138688)
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     1096
1196
2204
2304
2304
9463
9563
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 1095: contig of 1095 bp in length
1195: gap of unknown length
2203: contig of 1008 bp in length
2303: gap of unknown length
9462: contig of 7159 bp in length
9562: gap of unknown length
25807: contig of 16245 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Center
                                                                                                                                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 990315 Consensus quality: 133029 bases at least Q40 Consensus quality: 135140 bases at least Q30 Consensus quality: 13523 bases at least Q20 Insert size: 138187; sum-of contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: gtc-seqcenter@genomecorp.com
----- Project Information
Center project name: hg317
                                                                                                                                                                                                                                                                                              Quality coverage: 6.3x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.genomecorp.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: GTC
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 length
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AUTHORS
TITLE
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Best Local :
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249; Conserv
                                                                                                                                                           Homo sapiens chromosome 10 clone PROGRESS ***, 14 unordered pieces AL591464
                                                                                                                               AL591464.2 GI:17973978
HTG; HTGS_PHASE1; HTGS_1
                  Burton, J
                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           Homo sapiens
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                                       (sites)
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     Submission
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/chromosome="10"
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                                                       Chordata;
Primates;
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Db 134562 CATACCATGTATTTACTTTAAAAACAGAAAAAAAGACATGTATGGATATGTCTATTTTTT 134503
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68426. .13868
/note="assembly_name:Contig59"
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2304. .9462
/note="assembly_name:Contig55
ctone_end:T7"
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1196. .2203
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39972. .68325
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Pred. No. 2.1e-60;
; Mismatches 0;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SEQUENCING IN
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                                                                                                                                                                                                                       source
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 189117 bases at least Q40
Consensus quality: 192136 bases at least Q30
Consensus quality: 193772 bases at least Q30
Consensus quality: 193772 bases at least Q20
Insert size: 195074; sum-of-contigs
Insert size: 221513; 17.0% error; agarose-fp
Quality coverage: 4.57x in Q20 bases; sum-of-contigs Quality
coverage: 4.33x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanycr.cc.
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Dec 20, 2001 this sequence version replaced gi:14141513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bB302D10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ambridgeshire, CB10 ISA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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56769 6606
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66165 7410
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41024 52424: contig of 11401 bp in length
52425 52524: gap of 100 bp
52525 56668: contig of 4144 bp in length
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                 fragment_
52525. .5
                                                                                                                                  /clone="RP13-302D10"
/clone_lib="RPCI-13.2"
                                                                  /note="assembly_fragment:00704
fragment_chain:1"
41024. .52424
                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                      4 193323: gap of
4 196374: contig of
Location/Qualifiers
/note-"assembly_fragment:02444
                              /note="assembly_fragment:02076
fragment_chain:1"
                                                                                                                                                                  /chromosome="10"
                                                                                                                                                                                                                                                                                                                                                                 100 bp
100 bp
143238: contig of 8692 bp:
143238: gap of 100 bp
151820: contig of 8582 hm
151920: gap of
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56668: contig of 4144 |
768: gap of 100 bp
66064: contig of 9296 |
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193223: contig of
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134346: cont
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120523: contig of 2398 bp in length
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74102: contig of 7938 bp in length
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contig of 7679 bp
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contig of 13723 h
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9296 t
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Best Local Similarity
Matches 249; Conserv
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193324. .196374
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41071 c 41893 g
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143239. .151820
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fragment_chain:1"
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Patent: W
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An atypical PKC directly associates and colocalizes at the epithelial tight junction with ASIP, a mammalian homologue
                                                                                                                                                                                                                                                                                                                                                 Submitted (03-JUL-1997) Yasushi Izumi, Yokohama City University School of Medicine, Molecular Biology; 3-9, Fuku-ura, Kanazawa-ku, Yokohama, Kanagawa 236, Japan (E-mail:izumi@med.yokohama-cu.ac.jp, Tel:045-787-2597, Fax:045-785-4140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB005549.1 GI:3868777 asbp; atypical PKC specific binding protein. Rattus norvegicus cell_line:3Y1 cDNA to mRNA.
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                                                                                                                                                                                                                     Caenorhabditis elegans polarity protein J. Cell Biol. 143 (1), 95-106 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Izumi,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : WO 0194629-A 3448 13-DEC-2001;
Pharmaceuticals (US)
Location/Qualifiers
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                                                   /gene="asbp"
260. .4273
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/db_xref="taxon:9606"
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                                                                                                                                                                                    Location/Qualifiers
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                    /codon_start=1
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DRLIEVNGVDLAGKSQEEVYSLLRSYKMEGTYSLLVERQEARPIRYKNILPRGAAIQDGRLKAG
DRLIEVNGVDLAGKSQEEVYSLLRSYKMEGTYSLLVERQEARPHREMNAEPSQMQSP
KETKAEDEDIVLTPDGTREFLTFEVPLNDSGSAGLGVSVGRGNSKENHADLGIFVKSI
INGGAASKDGRLRVNDQLIAVNGESLLGKANQEAMETLRRSKSTEGNKRGMIQLIVAS
RISRCNELRSPGSPAAPELPIETELDDRERRISHSLYSGIEGLDESPTRNAALSRIMG
ESGKCQLSPTVNMPHDDTVMIEDDRLPVLPPHLSDQSSSSSHDDVGFIMTEAGTWAKA
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TISDSADCSLSEDDVDPVLAFGEFGRQSMSEKTDKGSNASQLDFVKTRKSKSMDLG
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SLERQMNGDPEKRDKAEKKDKAGKDKKKDREKEKDKLKAKKGLKGLGDMFFFFGKHR
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                                                                                                        SNHDRIQRLKQEFQQAKQDEDVEDRRRTYSFEQSWSSSRPASQSGRHSVSVEVQVQRQ
RQEERESFQQAQRQYSSLPRQSRKNASSVSQDSWEQNYAPGEGFQSAKENPRYSSYQG
SRNGYLGGHGFNARVMLETQELLRQEQRRKEQQLKKQPPADGVRGPFRQDVPPSPSQV
                                                      ARLNRLQTPEKGRPFYS"
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TFGCDDELLYGGMSSYDGCLALNARPQSPREGHLMDTLYAQVKKPRSSKPGDSNRSTP
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IFGSELGTNNVSAFRPYQTTSEIEVTPSVLRANMPLHVRRSSDPALTGLSTSVSDNNF
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/db_xref="GI:3868778"
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                                                                                                 Matches
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Best Local
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                                43
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                                                                                                 88;
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                                                                                                 Conservative
                                                                                                        28.1%;
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BASE COUNT ORIGIN

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            Norway rat.
                     HTG; HTGS_PHASE1.
                                AC103175.2 GI:17974664
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AC103175 168213 bp D Rattus norvegicus clone CH230-98H12, 74 unordered pieces. DNA linear
2, *** SEQUENCING HTG 21-DEC-2001 IN PROGRESS

Rattus

REFERENCE AUTHORS E 1 (bases 1 to 168213)

E 1 (bases 1 to 168213)

E Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

R Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,

Benton,J., Bhange,K., Blankenburg,K., Bonnin,D., Bouck,J.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

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Bowie,S., Brieva,M., Brown,E., Brown,M., Carron,T.F.,

Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,

Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,

Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,

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Dany,Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,

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Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,

Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,M., Ford,J.,

Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,

Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunarattee,P., Hale,S.,

Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A.,

Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Hale, S.,

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Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Kalisson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L. Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozado, R.J., Lu, E., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Petry, J., Peters, L., Pickens, R., Primus, E., Pu, L. L., Ouiles, M., Ren, Y., Rives, M., Rojusokan, I., Shooshtari, N., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stanek, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, N., Warlington, S., Walliams, G., Walliamson, A., Washington, C., Walliams, G., Williamson, A., Washington, C., Walliams, G., Williamson, A., Weczyk, R., Wooden, S., Wooley, K., G., and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24 NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 21, 2001 this sequence version replaced gi:17062822.

Center: Baylor College of Medicine Center code: BCM
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Worley, K.C.
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                                                                                                                                                                                                                                                                                               runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence as soon as it is available and the accession number wi
                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as the process of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                as soon as in
be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 136914 bases at least Q40 Consensus quality: 144233 bases at least Q30 Consensus quality: 150066 bases at least Q20 Estimated Insert size: 132552; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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5909: contig
6009: gap of
10545: contig
10645: gap of
14032: contig
14132: gap of
17936: gap of
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22214: contig
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26249: contig
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74 unordered pieces.
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Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Johnson, K., Jackson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Liu, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L.C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Marthiney, E., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Mouyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rutz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Wall, R., Wang, S., Walliams, G., Williamson, A., Washington, C., Walliams, G., Williamson, A., Washington, C., Weinstock, G. and Gibbs, R.
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Worley, K.C.

Direct Submission

Submitted (25-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Dec 20, 2001 this sequence version replaced gi:17064266.

On Dec 20, 2001 this sequence Version replaced gi:17064266.
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Consensus quality: 135039 bases at least Q40 Consensus quality: 141582 bases at least Q30 Consensus quality: 147182 bases at least Q20 Estimated insert size: 127529; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                   Center clone name: CH230-30D24
------Summary Statistics
Assembly program: Phrap; versi
                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgschelp@bcm.tmc.edu
Project Information
Center project name: GHQP
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JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

TITLE

COMMENT

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 74 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence as soon as it is available and the accession number be preserved. NOTE: Estimated insert size may differ from sequence length 7705 7805 13066 13166 13166 7704: contig 7804: gap of 13065: contig 13165: gap of 1329: contig 1929: contig 19329: gap of 19329: gap of unknown of 6064 of 7704 bp in length unknown length of 5261 bp in length length bp in] length bp in length length

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Protein binding and DNase-I-hypersensitive sites in the cis-acting regulatory region of the spore-coat SP96 gene of Dictyostelium Mech. Dev. 36 (3), 105-115 (1992)
                                                                                                     Dictyostelium discoideum prespore Dictyostelium discoideum
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GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 96842] from the original journal article.
                                                                                Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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length

of 2663

bp in l

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length

48089: 48189: 53727:

108531 110002 1111862 1111962 1113284 1113284 113384 113386 113386 117968 117968 117968 117968 117968 117968 117968

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of 1441
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101601 101701 104254 104354 106511 106611 108431

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87243 89380 89480 91425 91525 93038 93138 95351 96994

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                                                Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On May 25, 2001 this sequence version replaced g1:13606042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176741 bp
Homo sapiens BAC clone RP11-389E16
AC016732
                                                                                                                                                            Submitted (25-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-DEC-1999) Genome
University School of Medicine,
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The sequence of Homo sapiens BAC clone RP11-389E16
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Genome Res. 8 (11), 1097-1108 (1998)
99063792
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Sulston, J.E. and Waterston, R.
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               Center: Washington University Genome Sequencing Center Center code: WUGSC
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site: http://genome.wustl.edu/gsc
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nucleotide 182"
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52.1%;
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Center project name: H_NH0389E16
                                         Contact: sapiens@watson.wustl.edu
                           Summary Statistics
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence form more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise restriction digest. noted:

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. I
MCPherson, Department of Genetics, Washington University, St. I
MCPherson Department of Genetics, Washington University, St. I
MCPherson Department of Genetics, Washington University, St. I
Mapping Information:
Mapping Information washington University, St. I
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Mapping Information of Genetics, Washington University, St. I
McPherson, Department of Genetics, Washington University, St. I
McPherson, Washington University, Mapping Universi Louis

SOURCE INFORMATION:

donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Parark Cancer Institute (http://bacpac.med.buffalo.edu) VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the location. The clone sequenced to the left is RP11-261J9; the clone sequenced to the right is RP11-383T5. Actual start of this clone is at base position 1 of RP11-389E16; actual end is at base position 176741 of RP11-389E16.

the re are polymorphic base pair differences clone RP11-389E16 and RP11-261J9.
Location/Qualifiers in the overlap between

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8741. .9265
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968. .1087
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/clone_lib="RPCI-11"
140. .246
                                                                                                                                                                         /rpt_family="MER2_type" 2901. .2999
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/db_xref="taxon:9606"
/chromosome="2"
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               /rpt_family="Alu"
29621. 20668
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29197. .29496
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27823. .28134
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16873. .1
rpt_family-"AT_rich"
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16127. .16428
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18021. .18499
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10359. .10717
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10008. .10237
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Best Local Similarity 62.2%; Pred. No. 2.1;
Matches 61; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                            Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marguis, N., McEwan, P., McGurk, A., McKernan, K., McCandonald, P., Marguis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, Y., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zinmer, A., and Zody, M.
                                                                                                                  Submitted (09-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAR 1, 2000 this Sequence varion replaced gi:6957742.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 2, clone RP11-615C5 Unpublished
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1 (bases 1 to 203194)
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Homo sapiens chromosome 2 clone RP11-615C5 map 2, WORKING DRAFT
SEQUENCE, 32 unordered pieces.
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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
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30805. .30834
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30967 .31073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is ransitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                         28130 33133: contig of 5004 bp in length
33134 33233: gap of 100 bp
33234 37816: contig of 4583 bp in length
37817 37916: gap of 100 bp
37917 42224: contig of 4308 bp in length
42225 42324: gap of 100 bp
42325 48180: contig of 4308 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                       9732 9831: gap of 100 bp 11085 11184: gap of 100 bp 11185 1289; contig of 1253 bp in length 12900 12999; gap of 100 bp 13528 13627: contig of 528 bp in length 13528 13627: gap of 100 bp 13528 15214: gap of 100 bp 15215 16378: contig of 1164 bp in length 15215 16378: contig of 1164 bp in length 16379 16478: gap of 100 bp 18131: contig of 11653 bp in length 18132 18231: gap of 100 bp 18132: contig of 1852 bp in length 20184 20183: gap of 100 bp 100
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Center clone name: 615_C_5
Center Summary Statistics
Sequencing vector: M13; M77815;
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                                                48181 48280: gap of 100 bp in length 48281 54554; contig of 6274 bp in length 54555 54654; gap of 100 bp 54655 60966; contig of 6312 bp in length 60967 61066; gap of 100 bp 61067 71645; contig of 10579 bp in length 71646 71745; gap of 100 bp 71646 81326; contig of 9581 bp in length 71746 81326; contig of 9581 bp in length
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1492 1591: gap of 100 bp
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8196: con
gap of 100 bp
95: contig of 12569 bp in length
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128221 141049: cont.g of 12829 k
141050 141149: gap of 100 bp
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clone_end:SP6
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18232 20083
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28130. .33133
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/note="assembly_fragment"
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/chromosome="2"
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71746. .81326
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l. .1491
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                                                                                                                                                                                               Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 M Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15187187
Draft Sequence Produced by DOE Joint Genome Institute
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                     Submitted (15-AUG-2001) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                       www-shgc.stanford.edu
Quality: Phrap Qualit
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 88670 bases at least Q40 Consensus quality: 90162 bases at least Q30 Consensus quality: 91119 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 91895; sum-of-contlys
Insert size: 100858; 2.9% error; agaiose-fp
Quality coverage: 4.06x in Q20 bases; sum-of-contlys Quality
coverage: 3.74x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestesanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9214040.
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Center code: SC
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                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
7790: contig of 7790 bp in length
7791 7890; gap of
7891 19908: contig of 12018 bp in length
1990 20008: gap of
100 bp
26287: contig of 6279 bp in length
26388 26387: gap of
26388 46199: contig of 19812 bp in length
46200 46299: gap of
46300 54017: contig of 7718 bp in length
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Nakamura, Y., Isogai, T. and Sugano, S.
                                                                                                                                                                                                                                                                  Homo sapiens cDNA FLJ20754 fis,
            Unpublished (2000)
2 (bases I to 2696)
Sugano, S. Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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variant mRNA, complete cds.
AF196185
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NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA library sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Medical Science, Virology and Human Genome Center, Institute of Medical Science, Virology and Med
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="GI:7021051"
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/clone_lib="HEP"
/note="cloning vector pME18SFL3"
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gctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtgaaagctcag
                                                                                 gggatctcggtggctcccatcttccttcattgttctgaacatcctgtattgtaaaccatg
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밁

Conservative

100.0%; Score 249; DB y; 100.0%; Pred. No. 1.6e-60; O; Mismatches 0;

Length 5958; Indels

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Gaps

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Fang, C. and Xu, Y.

Direct Submission
Submitted (18-OCT-1999) Laboratory of Molecular and Cellular
Oncology, Shanghai Institutes for Biological Sciences, Chinese
Academy of Sciences, 320 Yue-Yang Road, Shanghai 200031, P.R. China
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Fang,C. and Xu,Y.
Exon/Intron Structure and Splicing Variants of a Novel Human
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RISKCHELKSPGSPGGELPIETALDDRERRISHSLYSGIEGLDESPSRNAALSRIMG
KYQLSPTVNMPQDDTVIIEDDRLPVLPPHLSDQSSSSSIDDVGFTVTADAGTWAAISRIMG
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SHDRIQRLROEFGOARQDEDVEDRRRTYSFEQPWPNARPATQSGRHSVSVEYQMQRQR
RNGYLGGHGFNARVMLETQELLRQEQRRKEQQMKKQPPSEGPSNYDSYKKVQDPSYAP
PKGPFRQDVPPSPSQVARLNRLQTPEKGRPFYS"
1395 c 1581 g 1358 t 1 others
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IFGSELGTNNVSAFQPYQATSEIEVTPSVLRANMPLHVRRSSDPALIGLSTSVSDSNF
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/protein_id="AAK27891.1"
/db_xref="GI:13491610"
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/db_xref="taxon:9606"
/chromosome="10"
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                                                                        GGGATCTCGGTGGCTCCCATCTTCCTTCATTGTTCTGAACATCCTGTATTGTAAACCATG 11094
                                                                                          gggatctcggttggctcccatcttccttcattgttctgaacatcctgtattgtaaaccatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-DEC-1996) Bioinformatics Division, Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA On Dec 9, 1998 this sequence version replaced gi:1773048.

Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing Technology. Data may contain low quality seq uence and BAC/Cosmid
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SEQUENCING IN PROGRESS ***, 1 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by the finished sequence as soon as it is available and the accession number will be preserved.

1 22279: contig of 22279 bp in length.
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L. and Smith, D.
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                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence will be replaced
                                                                                                                                                                                                                                                                                                                         /clone="CRI-JC2075"
5238 c 5397 g
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              /map="10p11.2"
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                                                                                                                                                                                                               Score 249; DB 2;
Pred. No. 1.8e-60;
; Mismatches 0;
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AL160409/c
                                                                                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requests: clonerequest@sanger.ac.uk

On Jul 19, 2001 this sequence version replaced gi:14625535.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submis sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                  IMPORTANT: This sequence is not the entire insert of clone RP11-406D17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP13-348N17 is at 104199 in this sequence. The true right end of clone RP11-490024 is at 2000 in
                                                                                                                                                                                                                                                                                                                                            http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HGP/Chr10

RP11-406D17 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10 constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sycamore, N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae;
1 to 106198)
                                                                                                          Location/Qualifiers
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/note="MIR repeat: matches 93.
1232. .1275 /note="MIR repeat: matches
989. .1039 /clone="RP11-406D17" /clone_lib="RPCI-11.2" 27. .160

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.139 of consensus" .144 of consensus

/note="22 copies 2

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14551. .14771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 104.
6646..6950
 /note="AluJo repeat: matches 1.
22502. .22739
                                                                                                                                                                                      /note="MLT1D repeat: matches 3..238 of consensus" 19087. .19391 /note="AluSq repeat: matches 1..310 of consensus" 19392. .19542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"MER57B repeat: matches 43.
10851 .10975
/note-"FLAM_C repeat: matches 15.
11451 .11758
                                                                                                                           /note="AluJo repeat:
20333. .20642
                                                                                                                                                           /note="MLT1D repeat:
19608. .19904
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/note="MLT1D 1
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6528. .6637
                                              'note="L2 repeat: matches 2414.
                                                                                               /note="AluSx repeat:
20670. .20956
                                                                                                                                                                                                                                                                      note="AluSg repeat:
                                                                                                                                                                                                                                                                                                      /note="AluJo repeat: matches 1. .292 of consensus"
17094. .17254
"mote="AluJo/FRAM repeat: matches 134. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                                        /note="LIMC4 repeat: matches 7728. .7834 | 16712. .1678. .7836 | 1678. .7836 | 1678. .7836 | 1678. .7836 | 16825. .17092
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER5A repeat: matches 34..189 of consensus 15868..15919
/note="26 copies 2 mer aa 73% conserved" 16133..16443
/note="AluSx repeat: matches 1..312 of consensus" 16599..16707
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8061..8354
/note="AluJb repeat: matches 1..289 of consensus"
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/note="MLT1J repeat: matches 1.
4648. .4815
/note="FRAM repeat: matches 4.
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note="Alujo/FRAM repeat: matches 152.
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                                                                                                                                                                          238. .501 of consensus
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               .311 of consensus"
                                              .2696 of
                                                                              .286 of consensus"
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В Ş

Matches

249;

Conservative

100.0%; Score 249; DB 9 100.0%; Pred. No. 2e-60; rative 0; Mismatches

DB 9;

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41103 .41726
/note="L1PA7 r
                  /note="LIPA7 repeat: matches 11.
51663. 51964
/note="Alundb repeat: matches 1.
51966. .52183
                                                                                       /note="AluSq repeat: matches 3.
44991. 45302
/note="Aluyo repeat: matches 1.
45536. .51640
                                                                                                                                                                                               /note="L1PA7 repeat: matches 5515. .6138 of consensus"
43386. .43747
                                                                                                                                                                                                                                                                                                         /note="AluSx repeat: matches 5. .302 of consensus" 39063. .39193
/note="PIAM_C repeat: matches 1. .131 of consensus" 39510. .39673
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37894. .38050
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34713..34840
note="109 copies 2 mer aa 69% conserved"
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38447. .38744
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER30 repeat: matches 1.
37547. .37852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33154. .33272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1MC4 repeat: matches 6940.
31133. .31547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10365..30644

10365..30644 repeat: matches

20645..31062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx repeat: matches 1. .239 23135. .23915 /note="TLIPA10 repeat: matches 5369. .27500. .27629
                                                                                                                                                                              'note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="L2 repeat: matches 2622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32592. .32686 note="TIMC4 repeat: matches 7791. .7972 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluJo/FRAM repeat: matches 178. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="AluJo repeat: matches 5. .282 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="LlPA6 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1MC4 repeat:
31648. .32167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="66 copies 2 mer aa 62% conserved"
30233. .30328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluJo repeat: matches 14 .153 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 80. .185 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="AluSq repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1MA3 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="48 copies 2 mer ta 65% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="MSTA_repeat: matches 1. .424 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .36155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .35654
                                                                                                                                                                                                                                                 repeat: matches 1497.
                                                                                                                                                                                                                                                                                    repeat:
                                                                                                                                                                                                                                                                                                                                                                                                matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            matches 1.
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                                                                                                                                                                                                                                                                                    matches 4. .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 6171. .6304 of consensus"
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                                     . 308
                                                                                                                                                                              .364 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                .188 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                .311 of consensus"
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                                                                                                        .304 of consensus"
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                                                                      .6145 of consensus"
                                                                                                                                                                                                                                                 .1667 of consensus"
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                                   of consensus"
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ORGANISM
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AC025823/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGATCTCGGTGGCTCCCATCTTCCTTCATTGTTCTGAACATCCTGTATTGTAAACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gggatctcggtggctcccatcttccttcattgttctgaacatcctgtattgtaaaccatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTATTGG 87853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (16-MAR-2000) Genome Therapeutics Corporation, 100
Street, Waltham, MA 02453, USA
On Apr 27, 2001 this sequence version replaced gi:9887686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC025823 138688 bp DNA linear HTG 24 Homo sapiens chromosome 10 clone RP11-60H16, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Data
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Mammalia; Eutheria;
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                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 138688)
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       1096
1196
2204
2304
2304
9463
9563
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1095: contig of 1095 bp in length
1195: gap of unknown length
2203: contig of 1008 bp in length
2303: gap of unknown length
9462: contig of 7159 bp in length
9562: gap of unknown length
9562: gap of unknown length
25807: contig of 16245 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Center
                                                                                                                                                                                                                                                                                           Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 133029 bases at least Q40
Consensus quality: 135140 bases at least Q30
Consensus quality: 13533 bases at least Q30
Consensus quality: 13633 bases at least Q30
Consensus quality: 13633 bases; at least Q30
Consensus quality: 13638 bases; sum-of-contigs
Quality coverage: 6.3x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: gtc-seqcenter@genomecorp.com
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: hg317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.genomecorp.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: GTC
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Therapeutics Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics
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AUTHORS
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VERSION
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AL591464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 134682 GGGATCTCGGTGGCTCCCATCTTCCTTCATTGTTCTGAACATCCTGTATTGTAAACCATG
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ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                              cataccatgtatttactttaaaaacagaaaaaaaaagacatgtatggatatgtctattttt
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                                                                                                                                                                                                                                                                                                                      TTTTATTGG 134494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249;
                                                                                                                                                                          Homo sapiens chromosome 10 clone RP13-302D10, *** SEQUENCING PROGRESS ***, 14 unordered pieces.
     Burton, J.
Direct Submission
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                               Homo sapiens
                                                                                                                 human
                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                   AL591464.2 GI:17973978
                                                                                                                                                                        AL591464
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25908
39872
39972
68326
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68426. .138688
/note="assembly_name:Cont1959"
. 30000 c 29755 g 37221 t
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/note="assembly_name:Contig57'
39972. .68325
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clone_end:SP6"
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clone_end:T7"
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/note="assembly_name:Contig15"
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/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_name:Contig14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 249; DB 2;
100.0%; Pred. No. 2.1e-60;
live 0; Mismatches 0;
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                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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                                                                     misc_feature
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 189117 bases at least Q40
Consensus quality: 192136 bases at least Q30
Consensus quality: 192772 bases at least Q30
Consensus quality: 193772 bases at least Q30
Insert size: 195074; sum-of-contigs
Insert size: 221513; 17.0% error; agarose-fp
Quality coverage: 4.57x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-DEC-2001) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coverage: 4.33x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                            187207
193224
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                /note="assembly_fragment:02076
fragment_chain:1"
52525..56668
                                                                                       /note="assembly_fragment:00704
fragment_chain:1"
                                                                                                                                          /clone="RP13-302D10"
/clone_lib="RPCI-13.2"
                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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note="assembly_fragment:02444/
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143238: gap of 100 bp
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134346: contig of 13723 h

    Project Information

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contig of 7679 bp
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contig of 43823 bp in length
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Sequence 3448 from Patent W00194629.
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fragment_chain:1"
66165. .74102
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56769. .66064
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41071 c 41893 g
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193324. .196374
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fragment_chain:3"
187207. .193223
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fragment_chain:2"
151921. .179327
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fragment_chain:2"
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fragment_chain:2"
15356
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fragment_chain:1"
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fragment_chain:1"
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                                                                                                                                                                                                                                    Izumi,Y., Hirose,T., Tamai,Y., Hirai,S., Nagashima,Y., Fujimo' Tabuse,Y., Kemphues,K.J. and Ohno,S.
An atypical PKC directly associates and colocalizes at the epithelial tight junction with ASIP, a mammalian homologue of Caenorhabditis elegans polarity protein PAR-3
J. Cell Biol. 143 (1), 95-106 (1998)
                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-JUL-1997) Yasushi Izumi, Yokohama City University School of Medicine, Molecular Biology; 3-9, Fuku-ura, Kanazawa-ku, Yokohama, Kanagawa 236, Japan (E-mail:Izumi@med.yokohama-cu.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asbp; atypical PKC specific binding protein. Rattus norvegicus cell_line:3Y1 cDNA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB005549.1 GI:3868777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB005549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete cds.
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                                                                                                                                                                                                                                                                                                                                                                               Tel:045-787-2597, Fax:045-785-4140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (sites)
                                                                                                                                                                                                                                                                                                                                                              (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism⇔"Homo sapiens"
/db_xref="taxon:9606"
89 c 88 g 10
                                                            260. .4273
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                       /gene="asbp"
                                                                            /gene=
                                                                                                                    /db_xref="taxon:10116"
/cell_line="3Y1"
                                                                                                                                                           /organism="Rattus norvegicus"
'product="atypical PKC
                    'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata;
Eutheria; Rodentia;
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                                                                                                   4273
                                                                        "asbp"
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Sciurognathi; Muridae; Murinae;
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specific binding protein"
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BASE COUNT ORIGIN

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RIJSRCMELRSPGSPAAPELPIETELDDRERTJSHSLYSGIEGLDESPTRNAALSRING
ESGKCQLSFTYNMPHDDTYMLEDDRELPVLPPHLSDQSSSSSHDDVGFLWFEAGTWAKA
TISDSADCSLSPDVDPVLAFQREGFGRQSMSEKRTKQFSNASQLDFVKTRKSKSMDLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVANNAPQALPRAPRLSOPPEQLDAHPRLPHSAHASTKPPTAPALAPPNVLSTSVGSV
YNTKRYGKRLNIQLKKOTEGLGFSITSBDVTIGGSAP IYVKNILPRGAAIQDGRLKAG
DRLIEVNGVULAGKSOEEVVSLLRSTKMEGTVSLLVFRQEEAFHPREMAAPFSQNOSP
KETKAEDEDIVLTPDGTREFLTFEVPLNDSGSAGLGVSVKGNRSKENHADLGIFVKSI
                                                                                                                                              SNHDRIQRLRQEFQQAKQDEDVEDRRRTYSFEQSWSSSRPASQSGRHSVSVEVQVQRQ
RQEERESFQQAQRQYSSLPRQSRKNASSVSQDSWEQNYAPGEGFQSAKENPRYSSYQG
                                                                                                                                                                                                                                            KDDKMEKMGRIKIQDSFTSEEDRVRMKEEQERIQAKTREFRERQARERDYAEIQDFHR
TFGCDDELLYGGMSSYDGCLALNARPQSPREGHLMDTLYAQVKKPRSSKPGDSNRSTP
                                            ARLNRLQTPEKGRPFYS"
                                                                                                  SRNGYLGGHGFNARVMLETQELLRQEQRRKEQQLKKQPPADGVRGPFRQDVPPSPSQV
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IIRGRGCNESFRAAIDKSYDKPMVDDDDEGMETLEEDTEESSRSGRESVSTSSDQPSY
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/db_xref="GI:3868778"
/translation="MKVTVCFGRTRVVVPCGDGRMKVFSLIQQAVTRYRKAVAKDPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRFEQAQHMFRQAMRARVIWFHVVPAANKEQYEQLSQREMNNYSPGRFSPDSHCVANR
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AUTHORS
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Nuzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulay, C., Earter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIGCATGCCTGTGGCACGAGGCCCTCCGTGTTCCCGCCGTTCATCTGTTGGTCTGAACAT 5392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC103175 168213 bp DI Rattus norvegicus clone CH230-98H12,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1.
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Pred. No.
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                                                       Hale, S.,
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Louiseged, H., Lozado, R.J., Lux., Lucier, A., Lucier, R., Luna, R., Ma.J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mein, G., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Nickerson, E., Nwokenkvo, S., Morgan, M., Nguyen, N., Nickerson, E., Nwokenkvo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Patcu, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Ward-Moore, S., Warland, R., Wang, S., Ward-Moore, S., Warland, R., Washington, C., Walliams, G., Williams, G., Williamson, A., Washington, S., Ward-Moore, S., Wung, S., Mu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Nareston, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Nareston, C., Sheret, S., Sheret, S., Stone, R., Washington, S., Walliams, G., Williamson, A., Washington, S., Ward-Moore, S., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Nareston, S., Walliams, G., Williamson, A., Washington, S., Nareston, S., Walliams, G., Williams, G., Walliams, G., R., Washington, S., Walliams, G., Williams, G., Walliams, G., 
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On Dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    findPhrapList
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission .
                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                        runs of \tilde{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                        as soon as i
be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 136914 bases at least Q40 consensus quality: 144233 bases at least Q30 consensus quality: 150066 bases at least Q20 Estimated insert size: 132352; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: GJKC Center clone name: CH230-98H12 ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                   158280 bp DNA linear HTG 20-DEC-Rattus norvegicus clone CH230-30D24, *** SEQUENCING IN PROGRESS ***, 74 unordered pieces.
                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Direct Submission
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'vorking draft' sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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                                  Protein binding and DNase-I-hypersensitive sites in the cis-acregulatory region of the spore-coat SP96 gene of Dictyostelium Mech. Dev. 36 (3), 105-115 (1992)
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Dictyostelium discoideum
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 GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq.96842] from the original journal article.
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Center project name: H_NH0389E16
                    Contact: sapiens@watson.wustl.edu
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between neighboring data submissions. clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap This sequence may not represent the entire insert of this

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998). An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) The clone sequenced to the left is RP11-261J9; the clone sequenced to the right is RP11-383I5. Actual start of this clone is at base position 1 of RP11-389E16; actual end is at base position 176741 of NEIGHBORING SEQUENCE INFORMATION:

There are polymorphic base pair differences the clone RP11-389E16 and RP11-261J9.
Location/Qualifiers in the overlap between

position 1 of RP11-389E16.

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FEATURES
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/db_xref="taxon:9606"
/chromosome="2"
                                       rpt_family="ERVL"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Castle, A., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Castle, A., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Gradyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Liu, G., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Timmer, A. and Zody, M.
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                                                                                                                      Submitted (09-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA (02141, USA on Mar 1, 2000 this sequence version replaced gi:6957742. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                    Direct Submission
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Birren, B., Linton, L.,
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                          Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       runs of \tilde{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 185000; agarose-fp
                                                               48181 48280: gap of 100 bp
48281 54554: contig of 6274 bp in length.
54555 54654: gap of 100 bp
54655 60966: contig of 6312 bp in length
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17746 100 b
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5115 15214: gap of 100 bp

5215 16378: contig of 1164 bp in length

6379 16478: gap of 100 bp

5479 18131: contig of 1653 bp in length

5132 18231: gap of 100 bp
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11184: gap of 100 bp
12899: contig of 1715 bp in length
12999: gap of 100 bp
13527: contig of 528 bp in length
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191: gap of 100 bp
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48180: contig of 5856 bp in length
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On Aug 30, 2001 this sequence version replaced gi:15187187.
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59; Conser
                                                                                                                                                                                                                                                                                                            4 (bases 1 to 119579)
DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                   Estimated Total Number of Errors
Location/Qualifiers
                                                                                                                                                     Quality: Phrap Quality >=40 99.9% of Sequence;
                                                                                                                                                                     www-shgc.stanford.edu
                                                                                                                                                                                       Finishing Completed at Stanford Human
                                                                                                                                                                                                         www.jgi.doe.gov
                                                                                                                                                                                                                                                                                              Direct Submission
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81427. .93995
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113980. .128120
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/db_xref="taxon:9606"
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103769. .113879
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Query Match

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Length 119579;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 88670 bases at least Q40
Consensus quality: 90162 bases at least Q30
Consensus quality: 91119 bases at least Q20
Insert size: 91895; sum-of-contigs
Insert size: 101858; 2.9% error; agarose-fp
Quality coverage: 4.06x in Q20 bases; sum-of-contigs Quality
coverage: 3.74x in Q20 bases; agarose-fp
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ALJS7035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requests: clonerequest@sanger.ac.uk
On Aug 12, 2000 this sequence version replaced gi:9214040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: dJ62B3
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Mammalia; 1
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
7790: contig of 7790 bp in length
7791 7890: gap of
100 bp
7891 19908: contig of 12018 bp in length
19909 20008: gap of
20009 26287: contig of 6279 bp in length
26388 26387: gap of
26388 46199: contig of 19812 bp in length
46200 46299: gap of
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Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk
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64730 69964: contig of 5235 bp in length
69965 70064: gap of 100 bp
70065 79016: contig of 8952 bp in length
79017 79116: gap of 100 bp
79117 82147: contig of 3031 bp in length
82148 82247: gap of 100 bp
82148 82247: gap of 100 bp
82148 92795: contig of 10548 bp in length.
Location/Qualifiers
1. 92795
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fragment_chain:1"
26388..46199
/note-"assembly_fragment:00189
fragment_chain:1"
46300..54017
/note-"assembly_fragment:00445
fragment_chain:1"
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/clone="RP1-6283"
/clone_lib="RPCI-1"
1. 7790
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fragment_chain:1"
82248. .92795
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fragment_chain:1"
64730. .69964
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fragment_chain:1
clone_end:SP6
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clone_end:T7
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fragment_chain:1"
70065..79016
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20009 .26287
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/db_xref="taxon:9606"
/chromosome="1"
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Listing first 45 summaries
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Plasmodium falcipa
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Human metastasis a	ABL34587	24	6351		₽.	æ
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S. epidermidis gen	AAH54988	22	3069		2	ü
DNA encoding novel	AAS83281	23	1804	•		Ö
Cat flea head and	AAC95256	21	500	•	.2	=
Tumour suppressor	AAS46696	22	5062	•	2	ō
Drosophila melanog	ABL13526	23	6398		۶,	9
Human immune syste	ABL34169	24	5914	13.1	32.6	æ
Human gene regulat	AAS61408	24	8032		2	7
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tumo	AAV83763	20	1704		33	ŭ
TNF	AAV34509	19	1704		33	4
Human TR2 receptor	AAA28149	21	881	•	33	ω
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Enterococcus faeca	AAX13154	20	8395		ω.	μ
Human immune/haema	AAK85746	22	6306	13.4	33.4	õ
Bovine-derived DNA	AAH21012	22	1267	•	ω.	٥
Nucleotide sequenc	AAF84800	22	110000			8
tococcus	AAV52167	19	13104		·w	7
immune	ABL34424	24	7784	٠	ω.	6
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otide s	AAZ25197	20	1900		34	ົວ
immune syst	ABL34425	24	7784			F
Human gene regulat	AAS61453	24	15416	•		0

ALIGNMENTS

RESULT AAF91875 immune system disorder; ALDS; autoimmune disorder; themour; inflammation; allergy; neurological disorder; theuratoid arthritis; inflammation; allergy; neurological disorder; ALDS; attoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Albelmer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kinney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification. 03-SEP-1999; 03-SEP-1999; 31-AUG-2000; 15-MAR-2001. WO200118022-A1. Homo sapiens. binding partner identification; Human secreted protein-encoding gene 18 cDNA clone HFPFK57, 22-MAY-2001 (first entry) AAF91875; AAF91875 standard; cDNA; 867 سر 2000WO-US24008. 99US-0152315. 99US-0152317. ΒP SEQ ID NO:28

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ARF91858-AAF91929 represent cDNAs corresponding to 52 human secreted cc AAB87414-AAB87454 represent human secreted protein fragments. The genes can defer corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene cherapy. Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the cc amount of the new genes. Specific uses are described for each of the cc series, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of c proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, callergies, neurological disorders (e.g., Alzheimer's disease, cancer stinding and evelopmental conditions. The proliferation of c sunburn, to maintain organs before transplantation, to gratinary tissues, to regenerate tissues, to identify their constants, and infections. The proteins can also be used to aid wound the primary tissues, to regenerate tissues, to identify their constants specific for a protein of the invention can be used in diagnostic immunosasays e.g., radioimmunosasay or enzyme linked immunosasays (ELISA). The present sequence represents a human cc secreted protein-encoding cDNA of the invention.
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Matches 249
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Soppet DR, Young
Moore PA, Shi Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preventing, treating or ameliorating Parkinson's diseases and cancers -
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J PE, Ebner I
, Wei Y, Flo
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Florence KA
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Pred. No. 2.9e-65;
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Olsen HS,
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Lafleur DW;
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21-DEC-1999;
14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
                                 5094
                                                                              5034
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                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic actis and encoded polypeptides are useful: to assess if a patient; is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                      4914
                                                                                                                                                                                                                                                                       Sequence 5510 BP; 1526 A; 1242 C;
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                                                                                                                                                                                                                                                                                      inhibiting cervicas curviseful for gene therapy.
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99US-0171350.
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2000US-0203791.
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                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclarosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5154
                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory, cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
  29-JAN-1998
                   AAT87468
                                     AAT87468
                                                468
                                                                                  Sequence
                                                                                                                                                                                                                                                                     Claim 1;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune system disease; cytosine methylation; antiasthmatic; teriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                              EPIGENOMICS AG
                                                                                                                                                                  7784
                                                                                                                                                                                                                                                                   SEQ ID NO 2397; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                           Piepenbrock
                                     standard;
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                              2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
 (first
                                                                                                                                                                  B₽;
                                                                                                                                                                  1776 A; 134 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                     DNA;
 entry)
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                                                                                                                             14.5%;
77.2%;
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                                                                                                                                                                                                                                                                                                                                            Berlin
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                                     ВP
                                                                                                                             Score 36.2;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                            <u>~</u>
                                                                                                                    Mismatches
                                                                                                                                                                  2219 G;
                                                                                                                                                                  3655 T;
                                                                                                                                     DB
                                                                                                                                     24;
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                                                                                                                                     Length
                                                                                                                    Indels
                                                                                                                                                                  other;
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bowel disease;
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                                                                                                                   Gaps
                                                                                                                    0
  The promoter has greater transcriptional activity than the herpes simplex thymidine kinase promoter and about the same as the {\sf SV40}
                         Cells containing the promoter of prodn. of heterologous proteins,
                                                       Claim
                                                                                                            WPI;
                                                                                                                                                                                                                       DE19539493-A1
                                                                                                                                                                                                                                                          misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHO; hamster; Ub/S27a;
                   Ovary cells.
                                                                                                                                               (THOM ) THOMAE GMBH KARL
                                                                                                                                                                  24-OCT-1995;
                                                                                                                                                                                   24-OCT-1995;
                                                                                                                                                                                                     30-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamster Ubiquitin/S27a
                                                                                                            1997-246232/23.
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                                                      25-26; Fig
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                                                                                                                              Enenkel
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813..861
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Nucleic acid containing promoter and hamster ubiquitin S27a gene - useful proteins, especially in CHO cells
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                                                                                                                                                                                                                                                       95DE-1039493
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/note= "polypyrimidine-rich sequence"
2374..2392
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/note= "promoter
2079..2400
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/note= "promoter
1868..2400
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739..2400
                                                                                                                                                                                                                                                                                                                                                                                  /note- "transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "polypyrimidine-rich sequence"
2418..2420
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/note= "homology with
2279..2302
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/note= "promoter
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1545..2400
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                                            22pp; German
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                                                                                                                                                                Gannon
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the Ub/S27a gene esp. in Chinese I
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                                                                                      regulatory regions of the for production of heterologous
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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1999;
18-MAY-1999;
13-SEP-1999;
17-SEP-1999;
                                                     The present invention relates to a recombinant DNA construct of a (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the construction of transgenic plant and animal cells expressing the constructs are useful for a construct of a constru
                                                                                                                                                                                                                    Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors fithe construction of transgenic plant and animal cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Centromere; michrosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC containing repeats from centromeres 1-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter
                                        factors,
                                                                                                                                                                                  Claim 102; Page 572-606;
                                                                                                                                                                                                                                                                                                                                                                                         (UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1999;
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                                 proteins such cytokines, ant
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99US-0127409.
99US-0134770.
99US-0153584.
99US-0154603.
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                                                                                                                                                                                                                                                                                                                                                 Keith
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                                    enzymes,
growth f
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`.76;
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                                    factors.
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139 ctgtgaatcccgatgtggaaaagctggaggtgaaagctcagcataccatgtatttactt 198

Query Match Best Local s Matches 61

Similarity 61; Conser

Conservative

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Score 35.2; I Pred. No. 0.79 0; Mismatches

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Matches 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57969
                                            can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of
                     dysplasia
                                                                                                                                                                                                Novel nucleic acids, treatment of disorder
                                                                                                                                                                                                                                                                        Endege WO,
Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene expression product; diagnosis; tumour; colon cancer colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer cell line
                                                                                                                                  AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from
                                                                                                                                                            Claim 15;
                                                                                                                                                                                   particularly cancers, especially colon
                                                                                                                                                                                                                                    WPI; 2000-087220/07
                                                                                                                                                                                                                                                                                                           (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                   10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                             09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperplasia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210
                                                                                                         human colorectal adenocarcinoma (colon cancer) cell line SW480. clones can be used to generate antisense oligonucleotides which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAAATTTTGTATAAATATTTTTA 57885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTTGAAAATAGTTTTTGTTATAACTACATATACGATTTATATATTTTCAAATCAAAA 57910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                     involving unwanted cell proliferation, such as or hyperplasia.
                                                                                                                                                          Page 361; 469pp;
                                                                                                                                                                                                                                                                        Steinmann
Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                             disorders
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                                                                                                                                                                                                                                                           J KE, A.
J, Derti A,
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rs involving unwanted cell
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rti A, Ford DM,
                                                                                                                                                           English.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SW480 cDNA clone SEQ
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No. 5
                                                                                                                                                                                                                                                                        Burgess CC, Bu
d DM, Lewis ME,
                                                                                                                                                                                   cancer
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                                                                                                                                                                                             proliferation
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                                                                                                                                                                                                            diagnosis
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                                  neoplasia,
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                                                                                                                                                                                                                                                                        JE;
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Best Local Similarity

14.0%; 53.7%;

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RESULT AAH17416
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                                                                            CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end complementary to a complementary to the CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence complementary to a CC coligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the CC particularly full-length cDNAs. The primers are also useful for the CC coll-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB35893 represent human cand sequences; AAB92446 to CC CAB95893 represent human amino acid sequences; AAB92446 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of the comprise of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 16860; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST
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Sugiyama
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakamatsu
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense
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, Otsuki
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                  (I) and (II) are useful for the development of vaccines against p. falciparum infection. (I) and polyvlonal antisera or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with p. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins can aid the identification of drugs to treat or prevent p. falciparum infection, or they can be used to identify drug resistance in p. falciparum. Sequencing of the plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expa our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1413
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vaccine and drug development. Parasite resistance to drugs and resistance to insecticides have led to a resurgence of malaria parts of the world, and there is a pressing need for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum; antimalaria; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA70246 standard; DNA;
                                                                                                                                                                                                                                                                                                                                         by chromosome 2 of the human malarial parasite, Plasmodium falciparum Also described are: (1) nucleotide sequences (II) encoding (I); and (vaccines against P. falciparum infection comprising (I) or (II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 558-559; 577pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-365347/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoffman S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes proteins and their fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carucci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US26796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 2;
protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human malaria parasite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasite,
and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ
                                                                                                                                                                                                 ne proteins)
falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO:379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds
                                                                                                                                                                                                                                                                                                                                                                                                                (I) encoded
                                                                                                                           to expand
                                                        mosquito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1352
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CCCCCCCCCCCCCX PYTTTTTX DXX PX PX PX PX PX X PX X PX X DX X PX X P

Sanaa

specifically mentioned within the specification.

protein sequences given in the present invention,

but which are not

Sequence 2364 BP; 1222 A; 247 C; 213 G;

682 T; 0

other;

and

drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide

Matches Query Match Best Local :

51;

Conservative

0; Pred. Score 34.8;

Mismatches

27; 21;

No. 1

DВ

2364;

Similarity

14.0%;

0

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RESULT
ABL34231
δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                       can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterioscierosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                          genes which are modified by the methylation of cytosines. The scan be used in the diagnosis and treatment of immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatLc; antiarthritic; antidabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                       Claim 1;
                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 2204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL34231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL34231 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1794
                                                                                                                                                                                                                                                                                                                                                                                                     03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1854
                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtctattttttttttatt 247
                                                                                                                                                                                                                                          2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTGAATTATTTTATT 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgaaagctcagcataccatgtatttactttaaaaaacagaaaaaaagacatgtatggatat 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAATTATCTGCATGAGATGACTTTAATTTATTATCATCAACAATAACATTTTTTTGATAT 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune system disease;
                                                                                                                                                      SEQ ID NO 2204; 32pp +
                                                                                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                   AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15416
                                                                                                                                                                                                                                                                       Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytosine methylation; antiasthmatic;
                                                                                                                                                      Sequence Listing;
                                                                                                                                                                                                                                                                       ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nootropic;
                                                                                                                                                       German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                               gene, useful
abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                         sequences
                                                                                                                           associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Sequence 15416

BP;

4742 A;

239 C;

3068 G;

7367

Τ;

0

other

preeclampsia, graft versus-host

present

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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
           Sposition to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardia disorders, haemophilia, solid tumours and cancer. Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                 The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The
                                                                                                                                                                                                                                                                                             New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1966
                                                                                                                                                                                                                                                                                                                                                                                             Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2026
                                                                                                                                                                         chemical
                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-017470/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-2001; 2001WO-EP03968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200177375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS61453 standard; DNA; 15416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tttaatttttgatattgatgaattaatattaaaatgtataggatagaatgttagtaagft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene regulation-associated gene oligonucleotide #408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene regulation-associated gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             EPIGENOMICS
                                                                                                                                                                     pretreatment converts cytosine bases unmethylated at the
                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
                                                                                                                                                                                                                                                    SEQ ID No 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gynecological; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                             AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.8%;
                                                                                                                                                                                                                                                                                                                                                                                              Berlin
                                                                                                                                                                                                                                                   26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34.4; D
Pred. No. 4.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 15416;
                                                                                                                                                                                                                                                                                                  immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                           genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT
ABL3442
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Best L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence included in the sequence data for this specification associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1966
                                                       genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                             Olek A,
                                                                                                                                                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                               02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antirheumatic; antiarthritic; antidiabetic; antipsoriatic; anatinflammatory; cancer; eye disease; arterlosclerosis; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2026
                                                                                                                               Claim 1; SEQ ID NO 2398; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                    WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acute myeloid leukaemia; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL34425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL34425 standard; DNA; 7784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15416 BP; 4742 A; 239 C; 3068 G; 7367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                         (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tttaatttttgatattgatgaattaatattaaaatgtataggatagaatgttagtaagtt 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgtgaatcccgatgtggaaaagctggaggtgaaagctcagcataccatgtatttacttt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Conservative
                                                                                                                                                                                                                                                                         EPIGENOMICS
                                                                                                                                                           methylation
                                                                                                                                                                                                                                             Piepenbrock
                                                                                                  invention provides a number of human immune system
                                                                                                                                                                                                                                                                                                   2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system
                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                              Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.8%;
                                                                                                                                                                                                                                              Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34.4; D
Pred. No. 4.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2398
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                                                                                                                                        (2) a method for the production of hydrogen by culturing the above blue-green alga under light irradiation; (3) a method for the production of hydrogen by culturing the above blue-green alga anaerobically and then under light irradiation; (4) a method for the production of hydrogen by reacting the above blue-green alga with an electron receptor; and (5) a method for the production of hydrogen by culturing the above blue-green alga anaerobically and then reacting it with an electron receptor. The method is mild to environment. The present sequence represents a nucleotide sequence from an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A method has been developed for the preparation of hydrogenase in whice a blue-green alga introduced by a recombinant vector containing a heterologous hydrogenase gene is cultured in a medium to form and accumulate hydrogenase in the microbe body. Also claimed are: (1) a blue-green alga introduced by a recombinant vector containing a gene having a Shine-Dalgarno sequence consisting of AAGGAA upstream of the hydrogenase structural gene derived from a Clostridium genus microbe; (2) a method for the production of hydrogen by culturing the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium; hy
Shine-Dalgarno;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AGEN )
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                                                                                                                                                     Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be
                             ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative discreters, graft-versus-host disease aging, glomerular disease, Lewy body disease, arthritis, arthritis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                        Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01ek
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06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
 Sequence 6298 BP;
                                                                                                                                                                                                                                                                                                                                             associated with cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200168911-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemically pretreated genomic DNA associated with cell cycle #32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2001; 2001WO-EP02945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS45358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS45358 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1771 CATAATGCTGTTTTATT 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mmunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtctatttttttttatt 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgaaagctcagcataccatgtatttactttaaaaaacagaaaaaaagacatgtatggatat 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTAAAATATTGATGTATTTCAAAAATGTATTATAATACAGCTTGATAAAAATTTAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATATAGTACAGTTTTTGTTGCATTTATAATAAAAACAGCATTATGAAAAAACAATATTTT 1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                           H
                                                                                                                                                                                                                                                                                                           ŏ
1583 A; 182 C; 1402 G; 3131 T; 0 other;
                                                                                                                                                                                                                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1832
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RESULT 14
AAH10129/c
Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
        sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH36742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA clone (3'-primer) SEQ ID NO:6964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH10129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH10129
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                                                                                                                                                                                                                                                                                                                                                        full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                                                                                                        3; SEQ ID 6964; 2537pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA;
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56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wakamatsu A,
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                           G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                          ROM; English.
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4.3;
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto
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RESULT 1
ABL32179
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Best Local
including eye diseases such as retinopathy, neuvasculus granter myeloid macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 represent oligonucleotides, of the present invention.
                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                              01ek
                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                 antlinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 540
                                                                                                                        Claim 1; SEQ ID NO 152; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                        (EPIG-)
                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                     02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                               03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                       WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                     neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL32179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL32179 standard; DNA; 5536 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gctcagcataccatgtatttactttaaaaacagaaaaaaagacatgtatggatatgtcta
                                                                                                                                                                                                                                                                                                                                                                                                                           ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                        EPIGENOMICS AG
                                                                                                                                                                                                                             Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                 2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                      2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 A; 123
                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid
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                                                                                                                                                                                                                              Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             all of
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Pred. No. 2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy;
bowel dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540;
                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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XX
SQ Sequence 5536 BP; 1644 A; 86 C; 1202 G; 2604 T; 0 other;
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Вb δÃ Query Match Best Local S Matches 41 Local Similarity Conservative 13.68; Score 33.8; D Pred. No. 4.7; 0; Mismatches 0 DB 12; 24; Indels Length 722 244 0; Gaps

0

Search completed: September 21, 2002, 10:16:45 Job time: 6276 sec

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Result
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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                                                                                                                                                                                                                                                                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on:
                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB seq
 28.8
28.8
28.4
28.4
                                                                           length:
                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_NA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                        US-09-757-781-21
249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383533 seqs, 122816752 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cagcggtggtggcaggaagc...
                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*./cgn2_6/ptodata/2/ina/5B_COMB.seq:*/cgn2_6/ptodata/2/ina/6A_COMB.seq:*/cgn2_6/ptodata/2/ina/6B_COMB.seq:*/cgn2_6/ptodata/2/ina/6B_COMB.seq:*/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*/cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                    Length DB
2658
524
4875
19124
279
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2622
2902
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2663
3252
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1724
          US-08-773-608A-1
PCT-US95-08295-22
US-08-460-739-1
US-08-487-826B-13
US-08-686-678A-50
US-08-521-4894
US-08-577-463A-1
US-08-577-463A-3
US-08-714-918-95
                                                                                                                                                                                                                         US-09-146-950-19
US-09-146-950-17
US-08-509-024-1
US-09-333-279-1
                                                                                                                                            US-09-146-950-1
US-08-309-024-6
US-08-33-279-6
US-08-339-304A-5
US-08-136-74-8B-3
US-09-118-442-1
US-09-677-064-1
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US-09-328-111-579
US-09-146-950-3
                                                                                                                        PCT-US96-12374-1
US-07-847-010-18
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(without alignments)
1573.521 Million cell updates/sec
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US-09-051-969A-5
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27.8	27.8	27.8	27.8	27.8	28	28	28	28	28	28	28	28.2	28.2	28.2	28.4	28.4	28.4
11.2	11.2	11.2	11.2	11.2	11.2		11.2		11.2	11.2	11.2	11.3	11.3	11.3	11.4	11.4	11.4
1002	1002	886	886	886	. 6124	2612	392	392	392	392	392	2075	618	618	5300	2902	2902
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US-09-073-898-43	US-08-960-780-43	US-08-569-063C-1	US-08-609-443B-1	US-08-469-427A-1	US-08-213-419B-3	US-09-105-390-7	PCT-US94-10529-8	US-08-950-449A-8	US-08-605-002A-8	US-08-250-975-8	US-08-469-421-8	US-08-238-163-3	US-08-352-902D-17	US-08-961-810-17	US-08-766-014-1	US-09-266-417-95	US-09-265-315-95
Sequence 43, Appl	Sequence 43, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 8, Appli	8	Sequence 8, Appli	Sequence 8, Appli	Sequence 3, Appli	Sequence 17, Appl	Sequence 17, Appl	Sequence 1, Appli	Sequence 95, Appl	Sequence 95, Appl

ALIGNMENTS

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; LOCATION: US-09-051-969A-5
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                                                                                                                                                                    TELEPHONE: 202-371-260
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
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                                               TOPOLOGY: li
MOLECULE TYPE:
FEATURE:
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US/0
FILING DATE: 1998-09-30
CLASSIFICATION: 435
                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: 202-371-2600
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: FLESHNER, RAZ E.
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSE: STERNE, KESSLER, GOLDSTEIN &
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NOE, WOLFGANG
TITLE OF INVENTION: INTENSIVE HOM
TITLE OF INVENTION: FROM HAMSTERS
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
CITY: W
STATE:
                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                 NAME/KEY:
                                                                                                   STRANDEDNESS:
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Score 36; Pred. No.

DB 3;

Length 2529;

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CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 579
LENGTH: 619
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US-09-328-111-579/c
: Sequence 579, Application US/09328111
; Patent No. 6262333
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; OTHER INFORMATION: n = A,T,C
US-09-328-111-579
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                                                 RESULT
  Sequence 3, Applica Patent No. 6287808
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Best Local
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APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E. APPLICANT: Carroll III, Eddie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Catino, Theodore J. APPLICANT: Derti, Adnan
                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                        412
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                    Application
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Pred. No. 0.039;
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  US-09-146-950-17/c ; Sequence 17, Application US/09146950A
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; ORGANISM: Homo sapiens US-09-146-950-19
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TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 579
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 591
TYPE: DNA
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TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/146,950A CURRENT FILING DATE: 1998-09-03 NUMBER OF SEQ ID NOS: 25
                                                                                                                                                             53 gggtctcgggggatctcggtggctcccatcttccttcattgttctgaacatcctgtattgt 112
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AGCCACACGCGCGTTCTCTGTCCT 337
                                 aagctcagcataccatgtatttact 197
                                                                                AAGCGCGGCACGCGCGCAGTGGTCCCCGTCCTGGACGATGCAGAAGTGGCCTGGGCTGC 362
                                                                                                                    aaaccatggctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtga 172
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Pred. No. 0.63
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-146-950-17
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Best Local S
Matches 74
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APPLICANT: SPERR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
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Best Local S
Matches 74
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APPLICANT: Busfield, Samantha J.
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                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/509,024B CURRENT FILING DATE: 1995-07-25 NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION: PROTEIN FAMILY AND USES '
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: U5/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
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les 74; Conserv
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Pred. No. 1.1;
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Pred. No. 1;
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; LOCATION: (297)...(875)
US-09-146-950-1
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APPLICANT: Busfield, Somantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REPERENCE: 09404/057001

CURRENT APPLICATION NUMBER: US/09/146,950A

CURRENT FILING DATE: 1998-09-03

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: 1929
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CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS
FILE REFERENCE: 0290-1
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                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1929
TYPE: DNA
ORGANISM: Homo sapiens
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AGCCACACACGGCGTTCTCTGTCCT 633
                                aagctcagcataccatgtatttact 197
                                                                    AAGCGCGGCACGCGCGCAGTGGTCCCCGTCCTGGACGATGCAGAAGTGGCCTGGGCTGC
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Pred. No. 1.1;
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US-08-509-024-6/c

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LENGTH: 4622;
TYPE: DNA;
ORGANISM: Homo sapiens
US-08-509-024-6
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APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I
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Best Local Similarity
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CURRENT FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
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CURRENT FILING DATE: 1995-07-25
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
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                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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173 aagctcagcataccatgtatttact 197
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                                                                        113 aaaccatggctggggtgctaaagtgcctgtgaatcccgatgtggaaaaagctggaggtga 172
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Pred. No. 1.7;
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Pred. No. 1.7;
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                                                                                                                                     RESULT 12
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Best Local S
Matches 43
                                                                  Sequence 3, Application US/08136743B Patent No. 5459063 GENERAL INFORMATION:
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NAME: NORMAN, OBLON F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 234
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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                                                                                                                                                                                                                                                        1701 ATGGGATAAATTTAACAAAAATGCTGAAAAAAGAGTTATTTGAGAATGTATAATTTTTT 1760
APPLICANT: Barry S. Cooperman, Harvey Rubin,
APPLICANT: Jerome Salem, and Alison L. Fisher
TITLE OF INVENTION: "plasmodium falciparum Ribonu-
TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide inhi
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LENGTH: 2646 base pairs
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TITLE OF INVENTION: FI
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                                                                                                                                                                                                                                                                                      182 ataccatgtatttactttaaaaacagaaaaaaagacatgtatggatatgtctatttttt 241
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CLASSIFICATION:
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SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP:
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43; Conservative
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SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: TH NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:

Thereof "

ADDRESSEE:

The University of Pennsylvania

3700 Market Street

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Best Local S
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Patent No. 6197561
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                          CURRENT APPLICATION NUMBER: US/09/118,442B CURRENT FILING DATE: 1998-07-17 EARLIER APPLICATION NUMBER: 60/055,446 EARLIER FILING DATE: 1997-08-11 EARLIER APPLICATION NUMBER: 60/055,526 EARLIER FILING DATE: 1997-08-08 EARLIER FILING DATE: 1997-07-28 EARLIER FILING DATE: 1997-07-28
                                                                                                                                                         TITLE OF INVENTION: Genes Controlling Phytate Metabolism TITLE OF INVENTION: Plants and Uses Thereof FILE REFERENCE: 0706
                                                                                                                                                                                                                       APPLICANT: Beach, Las
APPLICANT: Wang, Xun
                                                                                                                                                                                                                                                        APPLICANT: Martino-Catt, Susan J. APPLICANT: Wang, Hongyu
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INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720
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CLASSIFICATION: 435
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Local Similarity 63.9%;
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
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for Windows Version 3.0
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Pred. No. 2.8;
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US-09-118-442-1
                                                                                                                                            US-09-677-064-1
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Best Local Similarity
                                                             Matches
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PRIOR APPLICATION NUMBER: 09/
PRIOR APPLICATION NUMBER: 09/
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PRIOR FILING DATE: 1997-08-08
PRIOR APPLICATION NUMBER: 60/
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CURRENT FILING DATE: 2000-09-29
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                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                        LOCATION: (258)...(2666)

NAME/KEY: misc_feature
LOCATION: (1)...(3252)

OTHER INFORMATION: n = A,T,C
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NAME/KEY: CDS
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LOCATION: (258)...(2666
NAME/KEY: misc_feature
LOCATION: (1)...(3252)
                                                                                                                                                                                                                                                     ORGANISM: Zea mays
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TYPE: DNA
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1862 GTTCAAGGCACTCTTAAATATAGACGATTCTTGAGGCACAACTCCTGTTAGGAGAAGAGT 1803
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                92 gttctgaacatcctgtattgtaaaccatggctggggtgctaaagtgcctgtgaatcccga 151
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Pred. No. 3;
0; Mismatches
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Best Local Similarity 50.3%;
Matches 73; Conservative
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GENERAL INFORMATION:
APPLICANT: Northwestern University
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FEATURE:
NAME/KEY:
LOCATION:
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NAME: NOrthrup, Thomas E.
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: NOR3446P020PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5400
TELEPAX: (312) 616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1
MOLECULE TYPE:
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                   173 aagctcagcataccatgtatttact 197
                                                                                                   113
                                                                                                                               ANTI-SENSE:
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654 AGCCACACACGCGTTCTCTGTCCT 630
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                                                                714 AACGGCGGCACGCGCGCAGTGGTCCCCGTCCTGGACGATGCAGAAGTGGCCTGGGCTGC 655
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180 N. Stetson, Suite 4700
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294..1142
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Search completed: September 21, 2002, 10:17:28 Job time: 3753 sec

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249
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gb_est2:*
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A1079538 oz04e06.x
A1038061 ox21b05.x
A1038061 ox21b05.x
A1038061 ox21b05.x
BF679962 602154666
BE176440 RC3-HT058
AW242451 xm99304.x
A1333325 qq05b01.x
A1129988 qc50c03.x
BE176633 RC3-HT058
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A1150937 qy91b11.x
A110937 gt38b05.x
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A1739028 w134d09.x
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62	62	62	62		ω.	69	70	70	70.4	70.4	70.4	72	73	73	76	76	ა	76.6	78	79	81.6	82		0	N	130.2	
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AA794533 vu68f08.r	BB836719 BB836719	8 uy82e0	BBE	BB74936	888	5711 mc7	' EST212	8666 ox39	3386 UI-	-ID 8	3888 UI-	BE105642 UI-R-BX0-	ij.	BM391560 UI-R-DY0-	UI-R-C	x39f08.	AA759442 vw64f04.r	53324	98487 UI-R-	9) вр25001	BE666034 149038 MA	BF041786 BP250016A	BF039164 BP250008B	AA159020 zo57c03.s	AA909465 oll4f04.s	AI002564 og90g04.s

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ALIGNMENTS

RESULT

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	source	FEATURES					COMMENT	JOURNAL		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	AI079538/c
/Organism="Homo saptens" /db_xref="taxon:9606" /clone="TMAGE:1674370" /clone="TMAGE:1674370" /clone="TMAGE:1674370" /clone="TMAGE:1674370" /clone="TMAGE:1674370" /clone="Corgan: Liver conception fetus" /note="Organ: Liver and Spleen; Vector: pT7T3D (pharmacia) /note="Organ: L	1536	Location/Qualifiers	Seq primer: -40m13 fwd. ET from Amersham	Insert Length: 1447 Std Error: 0.00	IMAGE Consortium (info@image.llnl.gov) for further information.	This clone is available rovalty-free through LINE. Contact the	Contact: Robert Strausberg, Ph.D.	Unpublished (1997)	Tumor Gene Index	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	1 (bases 1 to 536)	Primates;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	EST.	AI079538.1 GI:3415789	AI079538	clone IMAGE:1674370 3', mRNA sequence.	oz04e06.xl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA	AI079538 536 bp mRNA linear EST 29-SEP-1998	

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RESULT 2
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                                                                                                                                             CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 779 Std Error: 0.00

Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 536)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurolc Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                   cDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                    Ph
                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                (CGAP/BTGAP), Tumo
Unpublished (1998)
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:2165307"
/clone_1ib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                David N. Louis, M.D., Myrna R.
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1 (bases 1 to 561)

NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                           High quality sequence stop: 465.
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/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                               /db_xref="taxon:9606"
/clone="IMAGE:1656945"
                                                                  /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                                                                                                       organism="Homo sapiens"
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Pred. No. 1.1e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249;
                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence
BF679962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF679962 626 bp n
602154666F1 NIH_MGC_83 Homo sapiens
                                                                                                                                      http://image.llnl.gov
Plate: LLCM1146 row: d column:
                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                         quality sequence stop: 621.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_83"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: prostate; Vector: pDNR-L
                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                             /clone="IMAGE:4295392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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Pred. No. 1.1e-51;
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248; Conserv
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.p1?t1-&t2-RC3-HT0585-160
300-022-d04&t3-2000-03-16&t4-1)
                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                         Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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BE176440.1 GI:8639169
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Pred. No. 2.7e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al Similarity 98.
                            CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                           Unpublished (1997)
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нigh
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 540)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone_lib="HT0585"
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Pred. No. 4.2e-50;
0; Mismatches 4
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                                                                                                                                                                                                         Anatomy Project (CGAP),
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; Homo.
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AI333325/c
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                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length; 782 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                qq05b01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1931593
                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 486)
                                                   High quality sequence stop: 447.
                                                                       Seq primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                                    Homo sapiens
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/organism="Homo sapiens
                                    Location/Qualifiers
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/clone="IMAGE:2692302"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
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Pred. No. 1.1e-49;
0; Mismatches 5
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                                                                Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                    Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prar I.M.A.G.E. Consortium DNA Sequencing by: Washington Univ
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 486)
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AI952086.1
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                                                                                                                                                                                               Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                   Seq primer: -40UP from Gibco
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             quality sequence stop: 413.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:5744396
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                                                                                                                                        Washington University
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                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the INAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
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1 (bases 1 to 545)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                  Site_2: Eco RI; 1st strand
oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Site_2: NotI; Cloned unidirectionally. Primer: C Library constructed by Life Technologies."

112 c 100 g 110 t
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the
                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1713028"
                                                                 /lab_host="DH1UB"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not i
                                                                                                                        /dev_stage="adult"
                                                                                                                                      /sex="female"
                                                                                                                                                       /clone_lib="Soares_pregnant_uterus_NbHPU"
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Lu28"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                    Madhidia, Machidia, Rolling, Martindia, R., Briones, M.R., Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Ragai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOilveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                       Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Ludwig Institute for Cancer Research
Ludwig Institute for Cancer Research
                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t2=RC3-HT0585-010
400-013-b05&t3=2000-04-01&t4=1)
                                                                                                                                                                                     Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE176633 687 bp mRNA linear RC3-HT0585-010400-013-b05 HT0585 Homo sapiens cDNA, BE176633.1 GI:8639362
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                                                                                                                                                                                                                                                                                                                               sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                           quality sequence start: 13 quality sequence stop: 657. Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
128 c 116 g 129 t
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                                                 1 (bases 1 to 463)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                                                                       cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R.
                                                                                                                                                                                                                                                                                                                                                                                      qy65f11.x1 NCI_CGAP_Brn25 mRNA sequence. A1356239
                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa;
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                                     High quality sequence stop: 444.
                                                                                                                                               Bonaldo, Ph.D.
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/organism≖"Homo sapiens'
                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Eutheria;
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RESULT 12
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Best Local Similarity
Matches 215; Conserv
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                        cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1094 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anat
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/db_xref="taxon:9606"
                                                                                                    Location/Qualifiers
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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
AI369277
                                                        CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 723 Std Error: 0.00
Seq primer: -40UP from Gibco.
                                                                                                                                                                         Bonaldo, Ph.D.
                                                                                                                                                                                                        Ph.D
                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                    (CGAP/BTGAP), Tumo
Unpublished (1998)
                                                                                                                                                                                                                                                                                   1 (bases 1 to 446)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute / National Institute of Neurola
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI369277 446 bp mRNA linear EST 17-MAR-1999 9Y91b11.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2019357 3',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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/lab_host="DH10B"
                                           Location/Qualifiers
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/clone_lib="NCI_CGAP_Kid5"
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Pred. No. 1.7e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 798 Std Error: 0.00
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qe68b05.x1 Soares_fetal_lung_NbHL19W
IMAGE:1744113 3', mRNA sequence.
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Unpublished (1997)
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1 (bases 1 to 436)
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/Clone="IMAGE:1744113"
/Clone="ISoares_fetal_lung_NbHL19W"
/Clone=lib="Soares_fetal_lung_NbHL19W"
/Clone=lib="Soares_fetal_lung_NbHL19W"
/Clone="ISoares_fetal_lung_NbHL19W"
/Clone="ISoares_fetal_lung_NbHL19W"
/Clone="ISoares_fetal_lung_NbHL19W"
/Clone="IMAGE:1744113"
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/db_xref="taxon:9606"
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Location/Qualifiers
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/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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Pred. No. 5.1e-39;
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1 (bases 1 to 427)

Hillier_L. Lennon,G. Becker,M. Bonaldo,M.F. Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Therry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Genome Res. 6 (9), 807-828 (1996)
                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
Insert Length: 1397 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 395.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9),
97044478
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AA293275.1
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
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/organism="Homo sapiens"
/db_xref="GDB:5936269"
/db_xref="taxon:9606"
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Search completed: September 21, 2002, 09:42:10 Job time: 5937 sec
                                                                                                                                                                                              Query Match 70.7%; Score 176; DB 9; Length 427; Best Local Similarity 100.0%; Pred. No. 1.5e-33; Matches 176; Conservative 0; Mismatches 0; Indels
                                                      427 CTCCCATCTTCCTTCATTGTTCTGAACATCCTGTATTGTAAACCATGGCTGGGGTGCTAA 368
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/sex="Female"
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